

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:10:02 ; Search time 49 Seconds

(without alignments)

5634.254 Million cell updates/sec

Title: US-10-005-480A-743

Perfect score: 4804

Sequence: 1 MESTLTLATEBQPVKRNLTKK.....QPVSEILQLKTYLPPTFETI 875

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

SPTREMBL 25::*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaea:*

ALIGNMENTS

RESULT 1
 Q99k07 PRELIMINARY; PRT; 565 AA.
 ID Q99k07; AC DT 01-JUN-2001 (TREMBLrel. 17, Created)
 AC DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 AC DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Similar to eucocneelotide pyrophosphatase/phosphodiesterase 3
 DE (Fragment).
 GN ENPP3 OR AI875438.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI TaxID=10990; OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strasbourg R.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RL DR EMBL; BC005527; AAH05527; 1; -.
 DR MGI; MGI:2143702; Engp3
 DR GO; GO:0004519; F:Endonuclease activity; IEA.
 DR GO; GO:0016787; F:Hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR002591; Phosphodiest.
 DR Pfam; PF01223; Endonuclease; 1.
 DR Pfam; PF01663; Phosphodiest; 1.
 DR SMART; SMO0477; NUC; 1.
 PT NONGER
 SQ SEQUENCE 565 AA; 63835 MW; 7179104F1863A04 CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB ID	Description
1	2540.5	52.9	565	1 Q99k07	Q99k07 mus musculus
2	2415	50.7	906	11 Q924C4	Q924C4 mus musculus
3	2191	45.6	874	13 Q7ZKNN	Q7ZKNN xenopus lae
4	1360	28.3	251	4 Q9NQ9	Q9NQ9 homo sapien
5	1263	26.3	817	12 Q9JTH1	Q9JTH1 fowlpox vir
6	1263	26.3	817	12 Q9T61	Q9T61 fowlpox vir
7	972	20.2	415	11 Q8CAF0	Q8CAF0 mus musculus
8	837	17.4	195	11 Q9IVZ7	Q9IVZ7 mus musculus
9	835	17.4	152	4 Q9HS15	Q9HS15 homo sapien
10	755.5	15.7	479	10 Q9FS13	Q9FS13 spinacia ol
11	746	15.5	274	4 Q723P5	Q723P5 homo sapien
12	743.5	15.5	496	10 Q9SU83	Q9SU83 arabidopsis
13	737.5	15.4	479	10 Q4274	Q4274 oryza sativa
14	713.5	14.9	457	10 Q8AWJ3	Q8AWJ3 arabidopsis
15	712.5	14.8	457	10 Q9SU82	Q9SU82 arabidopsis
16	680.5	14.2	461	10 Q9SU81	Q9SU81 arabidopsis

Query Match 52.9%; Score 2540.5; DB 11; Length 565;
 Best Local Similarity 81.1%; Pred. No. 3.1e-207;
 Matches 460; Conservative 53; Mismatches 51; Indels 3; Gaps 3;
 Qy 310 KAERPFTYMFEEPDSSGHAGGPYSARTVAKQYDHAEGMMLMEGLKORNLNQVNII 369
 Db 1 KADRPSPFTYVEEDSAGHSSGPVSAQVTKALQVDNAFGMMLMEGLKORNLNQVNIV 60

DT	01-OCT-2003 (TrEMBLrel. 25; Last annotation update)		
DE	Hypothetical protein		
OS	Xenopus laevis (African clawed frog).		
OC	Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Xenopodinae; Xenopus.		
CC	[1]		
NCBI - TaxID=	8355;		
RN	SEQUENCE FROM N.A.		
RC	TISSUE[Embryo];		
RA	Klein S.; Straubberg R.;		
RL	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; ECAI675; AAH44675; 1; -		
DR	GO; GO:0004119; Endonuclease activity; IEA.		
DR	GO; GO:0016787; Hydrolase activity; IEA.		
DR	GO; GO:0003876; Fatty acid binding; IEA.		
DR	GO; GO:0009117; Nucleotide metabolism; IEA.		
DR	InterPro; IPR001604; Endonuclease.		
DR	InterPro; IPR002591; Phosphodiester.		
DR	InterPro; IPR001212; Somaticoedit.		
DR	Pfam; PF01223; Endonuclease; 1.		
DR	Pfam; PF01663; Phosphodiester; 1.		
DR	Pfam; PF01033; Somaticoedit_B; 2.		
DR	PRINTS; PRO0022; SOMATOMEDINB.		
SMART	SM00477; NUC; 1.		
SMART	SM00001; SO; 2.		
DR	PROSITE; PS00524; SONATOMEDIN_B; 2.		
KW	Hydrothalic Protein.		
SEQUENCE	974 AA;	99650 MW;	7EAB4EC1D9FCE46 CRC64;
SQ	45.6% Score 2191; DB 13; Length 874;		
Query Match	Best Local Similarity 45.1%; Pred. No. 3 2e-177; Mismatches 409; Conservative 161; Indels 255; Gaps 14;		
Matches	4		
QY	15 KNTLKYKIACTVLLAVIVMSLGLGLGKR-----LEKOGSCRKC 58		
DR	4 KNSFSFHVKISLYTFAIGINVCLGFTANFRKRSEENDEGVASVLSDPWRSSGSKERC 63		
QY	59 FDASFRGLENCRDVACKDRGCCWDPEDTCYESTRIMCNKPRCGBTREASLSCSD 118		
DR	64 FELJEEAPACRCDNLCKSYNSCCDEIEHCLKTGREWECIKDRGBTNEENACHCS 123		
QY	179 CLOKDCADYKSVCGGTWSLBNCDTAQOSQCPCBDFLPVILSMSMDGRAEVLTYWD 178		
DR	119 KVNNDIDLRSCTTHSPMNPVPTKFPLNYLTAGLYPSHGGIVGNMSYDPVIDANFS 243		
DR	124 CLAKGDCTNYQVCKGTHADDCEBMKHECPAGFVRPLLIIFSDVGRASYNKKGH 183		
QY	179 LSSKEQNNPAWNHGQPWMULTAMYGLKAATYFWPGSEVATNGSFSTYMPYNGSYFER 298		
DR	184 KVNNDIDLRSCTTHSPMNPVPTKFPLNYLTAGLYPSHGGIVGNMSYDPVIDANFS 243		
DR	244 LRREKFNHRWNGQPIWITASQGLXATFPPW-----ERR 285		
QY	299 ISTLKHLDLPKAERPRFTYMFEEPDSGHAGGPYSARVIALQVHDHAFGMIMEGLKQ 358		
DR	286 IFTFLQWNLHPDNERPRFTYALSEPODQAGHGXGPFOPELAQKLKYNDLGKQ 345		
QY	359 RNIHNCVNLILLADHGMDQTYCNKMEYTDIFPRINFYMEGAPDRAHN-TIPHDFF 416		
DR	346 MKLHRCVNVIFVGDHGMEEATCERTEFLNSVNVDDFALLPGSIGMRMSRNPNKHD-- 403		
QY	417 SFNSEEIYRNLSGRKDPDHFKPYLTDPDKRHYAKNRVIDKVLFDQWMLAVRS--- 472		
DR	404 ---PKAVIANTIKPKDQHFKLQHPRKHYAKNRVIDKVLFDQWMLAVRS--- 460		
DR	473 -KSNTNCG_GGNHGYNNFRSMEAIFLHGPSFKKEKTEVEPPENIEVYNLMCDLIRIOPA 530		
DR	461 YRQQGKCAFQGDHYDNKTSMQLVFLHGPSFKYKVPPFENIEVYNLMCDLIRIOPA 520		
QY	531 PNTGTHGSUNLHLKVPFEPSHAEEVSKEVCFANPLP-----TESLDCFCPHLN 582		
DR	521 SNNTHGSLNHLRVAStKPAIPDEVSK-----PLPVTSPTVNEELGSC---DD 569		
QY	583 STQLEQVNQML-----NLTOQBETATATVK-----VNLPFGRRPVYQKNVDHCCLLYHR 628		
DR	570 KNRAEELNKRLYKGTDIVAVELNSEKELTSRNTDNLNLYGRPAVLY-KTYSVLSLHS 628		
QY	629 EYXSGFGKAMRMWNSSYTVPOLGDTSLPLPPTVPDCLRADYVPPSESQKCSFYLADKNI 688		
DR	629 DFEESGESEILMPWITSTKQADVSPIPEHUSNCVRLDPRAISPGNSQCSAYKADKQM 688		
QY	689 TIGGLYPPASNRTSDSQDALITSNLNUVMYEERKMDYFHSVLLKHTERNVNTVSG 748		
DR	689 SYGFLEPPQLOSSADSQYDAFLTNVTPYPAFKKINYFORLVKEPATERNGVNTVSG 748		
QY	749 P1FD3YDGHEDADEITKHLANTDVPPTPHYFVVLTSCKNSHTPENCPCGNLDVLPLII 808		
DR	749 P1FD3YDGVYDMKIKMFDVGSIPVPTHYYIISCMDNQAVNCDGCLSVSNTVSG 807		
QY	809 PHRPINVECSPEGKPEALWVEERTHAIAVRDVPEELITGLDFYQDQKVQPVSEILQLQTYL 868		
DR	808 PHRPDNEBONSBEESKVNEDLKLKHTTRIRDIELLTGLDFYRKTNRSYTEILSLKTYL 867		
QY	869 PTETUTI 875		
DR	868 HTYSEI 874		
RESULT 4			
Q9NQ99	PRELIMINARY;	PTT;	251 AA.
ID	Q9NQ99		
AC	Q9NQ99;		
DT	01-TRM-2000 (TRMBLrel. 15; Created)		
DT	01-OCT-2000 (TRMBLrel. 15; Last sequence update)		
DT	01-OCT-2003 (TRMBLrel. 25; Last annotation update)		
DB	DJ105H11.3 (Phosphodiesterase I/nucleotide pyrophosphatase 3) (Fragment).		
DB	DNM1		
GN	Human		
OS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCB_TaxID	9616;		
OX			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lovell J.;		
RL	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AL135914; CAB99214.1; -		
DR	GO; GO:0004519; Pyridonucleotide activity; IEA.		
DR	GO; GO:0003676; Pyridonucleotide acid binding; IEA.		
DR	GO; GO:0009117; Pyridonucleotide metabolism; IEA.		
DR	InterPro; IPR01604; Endonuclease.		
DR	IntePro; IPR01604; Endonuclease.		
PFam	PF01663; Phosphodiester.		
DR	SMART; SR00477; NUC; 1.		
NON_TER	NON_TER 1		
FT	251 AA; 28285 MW;	C726FD4719D480C CRC64;	
SEQID	251		
Query Match	28.3% Score 1360; DB 4; Length 251;		
Best_Local_Similarity	100.0%; Predict. No. 2; 7e-107;		
Matches	251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	472 SKSNTNCGGNGHGYNNFRSMEAIFLHGPSFKKEKTEVEPPENIEVYNLMCDLIRIOPA 531		
DR	1 SKSNTNCGGNGHGYNNFRSMEAIFLHGPSFKKEKTEVEPPENIEVYNLMCDLIRIOPA 60		
QY	532 NNGTGSILNLHKYFPEYSHAEVSKFSVCGFANPLPESLDFCPHLQNSTQLEQVHQ 591		
DR	61 NNGTGSILNLHKYFPEYSHAEVSKFSVCGFANPLPESLDFCPHLQNSTQLEQVHQ 120		
QY	592 MLNLTQEEITATVKNLPPGRPRVYLQKNDVHCLLYHREVSFGTAKRMPMWSYTVSQL 651		
DR	121 MLNLTQEEITATVKNLPPGRPRVYLQKNDVHCLLYHREVSFGTAKRMPMWSYTVSQL 180		

Qy	652 GDTSPPLPPTVDPCLRADVRVPPSEORKCSFYLADKNITHGFLYPPASNRSDSOYDALIT 711	Db	465 RVPIFDNIELLYNNCEILGINPANNNGTVGSILNLLNSRY -THVYSLDDITI----- 516
Db	181 GDTSPPLPPTVDPCLRADVRVPPSEORKCSFYLADKNITHGFLYPPASNRSDSOYDALIT 240	Qy	568 LPTESSLDC-----FCPHLQNSTLQBQVNQMLNLQTQBBITAVK---VNLPFGRRPVVLQ 617
Qy	712 SNLVPMPYEEFR 722	Db	517 ---ES-ECDRHAVGDDHUKKGCT-CKN1DRFSSKGKNEDSSRTRSSYYTINULPGKFAVLL 571
Db	241 SNLVPMPYEEFR 251	Qy	618 KNDVHCLLYHRETVSGFGRAMPMWSSYTVP-QLGTSPLPLPPTVDCLRADVRVPPSES 676
RESULT 5		Db	572 NRHHHC1LKNDNYVTAISKVNLPLWTSFSTDITYNTNLYNK---CYLQDMRVU-MYKV 627
Q9J5H1	PRELIMINARY;	PRT;	817 AA.
ID	Q9J5H1/		
AC	AC_09J5H1/_		
DT	01-OCT-2000 (TREMBrel. 15, Created)	Qy	677 QKCSFSYLLADKNITHGFLYPPASNRSDSOYDALITSNLVPMEEFRKMWDYFHSVLLKH 736
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)	Db	628 EPCRYSTSKQDVYGYLYPA--RATD-FQSILETTVTVMFENFKIWEMFMSLLEY 682
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)	Qy	737 ATERNGNVNVNSGPIDFDYNDGHDAPDBITKSLA-NNDVPIPTHYFVLTSCRNKSHTPE 795
DE	PFV030 alkaline phosphodiesterase.	Db	683 VQRGHVVNVMVGFEDNSNGI3RDSDTLMISGSGYNKVVIPSDYFVILTYCKDKDSL 742
GN	PFV030.	Qy	796 NCPGLWLDLVPFLPIPHRTNV-ESCP-BGKPEALWVEERFTIAHARDFVVELTGLDFYQD 853
OS	Fowlpox virus (FPV).	Db	743 DCYSNIKTESFVVPNSPTTNNCSRENITNTSYVVKIFSLHRVRKDIETVTSMSFYRN 802
OC	Avipoxviridae; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	Qy	854 KVOPVSEFLQLQKYL 868
OX	NCBI_TaxID=10261;	Db	803 VYXTSSNAYLKTWY 817
RN	SEQUENCE FROM N.A.		
RX	Afonso C.L., Tuiman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; RT "The Genome of Fowlpox virus.", J. Virol. 74:3815-3831 (2000).	RESULT 6	
RA	SEQUENCE FROM N.A.	09761	PRELIMINARY;
RA	Afonso C.L., Tuiman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;	ID	09761;
RA	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.	AC	09761;
RA	EMBL: AF198100; AA#4374.1; -	DT	01-NOV-1998 (TREMBrel. 08, Created)
DR	GO: GO:0015619; F:nucleic acid binding; IEA.	DT	01-NOV-1998 (TREMBrel. 08, Last sequence update)
DR	GO: GO:0016787; F:hydrolase activity; IEA.	DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)
DR	GO: GO:003676; F:nucleic acid binding; IEA.	DE	Alkaline phosphodiesterase I (EC 3.1.4.1).
DR	DR InterPro: IPR000591; P:nucleotide metabolism; IEA.	GN	PC1.
DR	DR InterPro: IPR000591; Endonuclease.	OS	Fowlpox virus (FPV).
DR	InterPro: IPR000591; Phosphodiest.	OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
DR	PFam: PF01663; Phosphodiest; 1.	OC	Avipoxvirus.
DR	SMART: SM00477; NUC_C; 1;	OX	NCBI_TaxID=10261;
SQ	SEQUENCE 817 AA; 94038 MW; 8404FD00641DA022 CRC64;	RN	[1]
Query Match 26.3%; Score 1263; DB 12; Length 817;		RP	SEQUENCE FROM N.A.
Best Local Similarity 36.9%; Pred. No. 2.6e-98; Matches 271; Conservative 145; Mismatches 279; Indels 40; Gaps 18;		RC	STRAIN=FP-9;
Qy	149 QSQCPFEFDLPPVLFMSMDGPFRAEYLWTDLMPNINKLKTGTHSKYKMBAMYPTKTFEN 208	RX	MEDLINE=98325194; PubMed=9658122;
Db	108 QVTCPPPERPPLIAMIANGPRDYLNWKWVYIPTKIDLMEHGTVIAP-KRPVYPTINTFN 166	RA	Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.; RT "Fowlpox virus encodes homologs of cellular alpha-SNAP, PC-1 and an orphan human homolog of a secreted nematode protein."; RL J. Virol. 72:6792-6795(1998).
Qy	209 HYTIIVGLYPESHGIDDNNNYDVNLNKNFSSKSEONNPWMMHGPMMULTAMYOGLKAAAT 268	DR	EMBL; AJ006408; CAA07014.1; -
Db	167 LYSIVTGLYPISHGTIDTNEFIDRGTDIEFTIASBETEEVWEGEPINTTMNGEKSAT 226	DR	GO: GO:0005159; F:endonuclease activity; IEA.
Qy	269 YFWPGSEVAINGSFPTIYMPNGSYUFPEERINTVRLWKLWDTGGRPYFVAYLEEPGSSG 328	DR	GO: GO:0016787; F:hydrolase activity; IEA.
Db	227 FFWPGSDKXVPRKRPTSYKSYEERINTVRLWKLWDTGGRPYFVAYLEEPGSSG 286	DR	GO: GO:0003676; F:nucleic acid binding; IEA.
Qy	329 HAGGPVSARVIKALQVVDHAGMGMELQKRNHLNCVN1TILLADHGMDDTQYCNKMEYNTD 388	DR	GO: GO:0004528; F:phosphodiesterase I activity; IEA.
Db	287 YEYGTDDERVKALEVKD1KALMKGKLQDQGLCANLILVSDHGMNSVDPKIVNLKD 346	DR	DR InterPro: IPR006404; Endonuclease.
Qy	389 YFPRINFFYMEGGPAPRIRAHNIPHDFSPNSEEIVRNLSCKRDPHQHKPLTBDLPKRL 448	DR	DR InterPro: IPR005591; Phosphodiest; 1.
Db	347 YITN-NDVVKPQGPATPKVQNLH-IRLDYDGIISSITSVCMDDQPFVSYSRSLPQL 404	DR	SMART; SM00477; NUC; 1.
Qy	449 HYAKNVRIDKVHFLWDQWLAVRSKSN-TMCGGGNHGHGYNNEFRSMEAIFIHALGCFSFKEKT 507	DR	SEQUENCE 817 AA; 94004 MW; CB69DA0508CC568B CRC64;
Db	405 HYSGSPFTEIGVYLEBQWQSTDENGNLKRSGGHGSDSFQMTAVLGYGAFLDV 464	DR	Query Match 26.3%; Score 1263; DB 12; Length 817;
Qy	508 EVEPFENIETYNNCMCDLRLRIOPAPNGTHGSNLHLLKVPFYEPSHAEEVSKPSVGFANP 567	DR	Best Local Similarity 36.9%; Pred. No. 2.6e-18; Matches 271; Conservative 145; Mismatches 279; Indels 40; Gaps 18;
Db	167 LYSIVLGLYPISHGIRDNEFIDRGTDIEFTIASBETEEVWEGEPINTTMNGFKSAT 226	Qy	149 QSQCPFEFDLPPVLFMSMDGPFRAEYLWTDLMPNINKLKTGTHSKYKMBAMYPTKTFEN 208
Db	108 QVTCPPPERPPLIAMIANGPRDYLNWKWVYIPTKIDLMEHGTVIAP-KRPVYPTINTFN 166	Qy	209 HYTIIVGLYPESHGIDDNNNYDVNLNKNFSSKSEONNPWMMHGPMMULTAMYOGLKAAAT 268
Qy	508 EVEPFENIETYNNCMCDLRLRIOPAPNGTHGSNLHLLKVPFYEPSHAEEVSKPSVGFANP 567	Db	167 LYSIVLGLYPISHGIRDNEFIDRGTDIEFTIASBETEEVWEGEPINTTMNGFKSAT 226

Qy	2659 YFWPGSEVAINGSFPSIYMPYNGSVPPERFERTISLLKWLKAERPRFTMYFEEDDSG	328	DR Pfam; PF01663; Phosphodiester; 1.
Db	227 FFGESDKVPRKRPTMVRSTNKSVPYERINTVRLWLMQDGYRYFYALYLEEFGSSG	286	DR Pfam; PF01033; Somatomedin_B; 2.
Qy	3229 HAGPVSVSIALQWVTHAFGMIMEGSIKLQRNLHNCVNTILLADHEMDQTCNCNKEYMTD	388	DR PRINTS; PS0024; SOMATOMEDIN_B; 2.
Db	287 YEGTDDDRVGKALEKVRKDALILMKGKDQLIGCANLILVSDHMSNVDPKKLVNLKD	346	DR SMART; SM00201; SO; 2.
Qy	3889 YFPRIINFYMEGSPAPIRAHNIPHDFFSNBETIVNLSCKPDKDHFKPLTPDLPKRL	448	DR PROSITE; PS0024; SOMATOMEDIN_B; 2.
Db	347 YLTN-NDVVIKPGATPVKPNLKH-IRLFVDGIISSTSVCMDDQPFPIYSRSRIPKRL	404	DR SEQUENCE; 415 AA; BC49A7742C6A3B60 CRC64;
Qy	3209 HAGPVSVSIALQWVTHAFGMIMEGSIKLQRNLHNCVNTILLADHEMDQTCNCNKEYMTD	388	Query Match 20.2%; Score 972; DB 11; Length 415;
Db	287 YEGTDDDRVGKALEKVRKDALILMKGKDQLIGCANLILVSDHMSNVDPKKLVNLKD	346	Best Local Similarity 41.0%; Pred. No. 5.7e-74; Matches 172; Conservative 72; Mis matches 124; Indels 52; Gaps 4;
Qy	347 YLTN-NDVVIKPGATPVKPNLKH-IRLFVDGIISSTSVCMDDQPFPIYSRSRIPKRL	404	DR Sequence 17: Conservatve 72; Mis matches 124; Indels 52; Gaps 4;
Qy	3209 HAGPVSVSIALQWVTHAFGMIMEGSIKLQRNLHNCVNTILLADHEMDQTCNCNKEYMTD	388	DR 3.2 LIVMSLGLGLG---LRKLE-----KQGSCRKCPDASFRGLENCR 70
Db	287 YEGTDDDRVGKALEKVRKDALILMKGKDQLIGCANLILVSDHMSNVDPKKLVNLKD	346	DR 15 LFTFAFLGNICLGPATASRINKRAENDEGPPTVLSDSPWTNTSGSCKGRCPFLQEVGPPPCR 74
Qy	508 EVERPFENEVYNNMCUDLRIQPAPIQPAPIQPAPIQPAPIQPAPIQPAPIQPA	567	DR 71 CDVACKDRGBCCWDFEDTCVESTRIWMCNKFRCGBTRLEASLCSDDCQKEDCADYK 130
Db	465 RVPIDNELYNNMCCEIGLGINPANNINGVGSUNLNIRNSR--THVSSLDTITI-----	516	DR 75 CDNLCKSYSSCCHDFDELCKTARGWECKDRGEVRENEACHSEDLSRGDCCTNYQ 134
Qy	568 LPTESDLDC----FCPHLQNSTOLEQVNQMNLTQEBITATVK-----VNLPFGRPRVLQ	617	DR 75 SVCGCETSVLEENCTAQOSQCPEGFDLPPVILFSMDGFRAYELTWDTLMNPINKLKTIC 190
Db	517 --ES-EDCRHAVGDKCT-CRNKDRFSEKGKNGEDSSRTRSSYYVNLPGFPAVIL	571	DR 135 VVCRGESBWHDDECEIRVPECPAGFVRDPLIIFSVDGRASYNKGSKMPNJEURSC 194
Qy	618 KVDHCLLYHREVSFGKAVMRPMWSSYTVP-QLGDTSPPLPTVPCDLRDAVRVPPSES	676	DR 191 GHHSKYMARMYPTKTFPNHYHTIVTGGYPESHGIIIDNNMYDVNLNKNSLSSKBNQNPWN 250
Db	572 NRHHHCITKDNTVTAVKNRNLPLWTSFSIDITYNSTNTYNTK---CYLQDMRV-MYVK	627	DR 195 GTHAYMRRPVPTKTFPNHYLTATGLGPYPSHRGIVGNSYDPPVDEATFLRGREKFHNHW 254
Qy	677 QKCSFYLLADKNTTHGFLPPASNRTSISQYDALTSLVPHYEERFKMWDYFHSVLLIKH	736	DR 251 HQGPMLWLTAMYQGLKAAUTFWPGSEVAINGSFSSYIIMPYNGSYFPERFISTLKLWLDPK 310
Db	628 EPGRYSYSTOKDVTGGLYPA--RATD-FQSLLIENTPVNPYRFKKWVFMSSLLIEY	682	DR 255 GGQPLWITATKQGYRAGTFEW-----SVSPHERRLTILQWSLUPD 296
Qy	737 ATTRNGVNVVSGPIFDYNDGHFADPDEITKHLA-NTDVPIFTHYFVVLTSCKNKSHTPE	795	DR 297 NERPSVYAYSEQDFSGHKYGPFGPEMTNPLREIDKTVGQLMDLGQLKLHRCVNVLIVF 356
Db	683 VQGHAVVTVAVGPFVDFDSNGFRDSLWILISHMSGYNNKVIVPSDIFTVILTCRDSSLN	742	DR 371 ADHGMDQTYCNCMEYMTDFPRINFYMEGGAAPRIRAHNIPHDFFSFNSEEIVRNLSSCR 430
Qy	796 NCFGWLDYLPFLPFRSTNV--ESCP-EKGPEALWVERFTAHARYDVEELLGTDFYQD	853	DR 357 GDHGNEVDTCRDTFELSNLYNTNVDDITLVPTGLRIR-----PKIPNLLKCFK 403
Db	743 DCYSNIKTESFVPPNSDYYNESCSRLENITSVSYVRKFSLHRVTKDIEVTWSMFSYRN	802	DR
Qy	854 KIQPVSEELQKTYL	868	RESULT 8
Db	803 VRTISSNNVAYLKYM	817	Q91VZ7 PRELIMINARY; PRT; 195 AA.
QCAFO	PRELIMINARY;	PRT;	ID Q91VZ7 PRELIMINARY; PRT; 195 AA.
AC	Q8CAFO_	PRT;	AC Q91VZ7 PRELIMINARY; PRT; 195 AA.
DT	01-MAR-2003 (TREMBLre).	23, Created)	DT 01-DBC-2001 (TREMBLre. 19, Created)
DT	01-MAR-2003 (TREMBLre).	23, Last sequence update)	DT 01-JUN-2003 (TREMBLre. 19, Last sequence update)
DT	01-MAR-2003 (TREMBLre).	25, Last annotation update)	DT 01-JUN-2003 (TREMBLre. 24, Last annotation update)
DE	Ectonucleotide Pyrophosphatase/Phosphodiesterase 2.		DB Similar to alkaline phosphodiesterase.
GN	ENPP2.		GN ENPP3.
OS	Mus musculus (Mouse).		OS Mus musculus (Mouse).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;		OX NCBI_TaxID=10090;
RN	SEQUENCE FROM N_A.		RN [1].
RP	SEQUENCE FROM N_A.		RP Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RC	SEQUENCE FROM N_A.		RC MGD; MGI:2143402; Enpp3.
RC	STRAIN=C57BL/6J; TISSUE=Hypothalamus;		RC GO; GO:0016787; Phosphodiester activity; IEA.
RX	MEDLINE=2235-683; PubMed=12466851;		RC GO; GO:0009117; P-nucleotidase metabolism; IEA.
RA	The FANTOM Consortium,		RA InterPro; IPB002591; Phosphodiester.
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;		RA InterPro; IPB001212; Somatomedin_B.
RT	"Analysis of the mouse transcriptome based on functional annotation of		RT DR Pfam; PF01033; Somatomedin_B; 2.
RT	60,770 full-length cDNAs.",		RT DR SMART; SM00201; SO; 2.
RL	Nature 420:563-573 (2002).		RL DR InterPro; IPR001212; Somatomedin_B.
DR	EMBL; AK038940; BAC30174.1; -.		DR DR PROSITE; PS0024; SOMATOMEDIN_B; 2.
DR	GO; GO:00016787; Phosphodiester activity; IEA.		DR DR SEQUENCE; 195 AA; D64F2CB37EPE4A65 CRC64;
DR	InterPro; IPR002591; Phosphodiester.		DR DR GO; GO:0009117; P-nucleotide metabolism; IEA.
DR	InterPro; IPR001212; Somatomedin_B.		DR DR InterPro; IPR001212; Somatomedin_B.

QY	1	MESTLTLATEQPKKNTUKKYKIACTVLLALIVINSIGLGIGLGLRKLEQSGCRKKCFD	60	OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Db	1	MDSRLALATEEPIKKDKSLKTKILKILVLLALIVINSIGLGIGLGLRKPERQSGCRKKCFD	60	OC Caryophyllales; Amaranthaceae; Spinacia.
QY	61	ASPRGLENCRDVACKDRGDCWDFDTCVESTRIMCNKRCGETRLEASLCSDDCL	120	RN [1]
Db	61	SSHRGLEGRCDGSGCTGRGDCWDFDTCTVCKSTO1WTCNLFRGENRLEFAKSCADDCL	120	RP SEQUENCE FROM N.A.
QY	121	QRKDCCADYKSVQCGETSWLBEECNDAQQSQCQPFMDGFRAEYIYTWDTL	180	RA Sonoda M., Ide H., Sato T., Nakagawa H.; RT "Cloning and deduced amino acid sequence of a nitrate reductase inactivator (NRI) from spinach leaves identifies a nucleotide pyrophosphatase"; RT Submitted (SBP-1999) to the EMBL/GenBank/DBJ databases.
Db	121	QRKDCCADYKTVQCGESPWVTEACASSQEPQCQPGFDLPPVILFMSMDGFRAEYLOQTWSL	180	RL EMBL; AB032413; BAB20681.1; DR GO; GO:0016787; F:nucleotide metabolism; IEA.
QY	181	MPIINKLKTKC 191		DR GO:0009117; P:nucleotide metabolism; IEA.
Db	181	LPNINKLUSKG 191		DR InterPro; IPR002591; Phosphodiester; 1. DR Pfam; PF01633; Phosphodiester; 1. DR Sequence 479 AA; 53122 MW; 14B8C05F4FB6FF94 CRC64;
QY	Q9H515	PRELIMINARY;	PRT; 152 AA.	Query Match Score 755.5; DB 10; Length 479;
AC	Q9H515_	Created)		Best Local Similarity 41.1%; Pred. No. 1 8e-55;
DT	01-MAR-2001	(TREMBLrel. 16, Created)		Matches 164; Conservative 63; Mismatches 141; Indels 31; Gaps 8;
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		QY 159 PPVILPSMDGFRAEYLTYWTDLMPNINKLKTGIGHSY-MRAMYPTKTFPHHYTIVTGYL 217
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		Db 94 PIVLISSDGFRGYQKAPT -PNHFLRNLNGTSAILGLIPVPEPLTFPHHYTIVTGYL 151
DE	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		QY 218 PESIGGIINNNMDVNLAQKNSLSSKEENNPANWKGQMMWLTAMYQGLKAATYFWPOSEV- 276
ENPP3,	DE	(Fragment).		Db 152 PPHGIGIINNNYFVDPTIKPSKMSHE --PKWNLGEELWETVAKIGKKAATYFWPOSEV- 208
OS	Homo sapiens (Human)	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]		QY 277 AINGSPFSIY-MPYNGSYVPEERLSTLWKLDPKARERPREYTMPEBPDSSGHAGPVS 335
NCBI_TAXID=9606;	RN			Db 209 KPDWDCPANCYCHNGSPFERVUTVSYFPLNIEPVMTLYEDBPHQHGQVGPDD 268
RP	SEQUENCE FROM N.A.			QY 336 ARVTKALQVVDIAGFMMEGKORNLLNCVNNTLADHGMDOCTYNRMEMYTDYFRINF 395
PA	Key M.;	Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.		Db 269 PEITQAVINNDMIGRILKIGLKGVRGVEDUNIFMVGHGMVGTCDKKLIFLDLIPSNW 328
DR	EMBL; AL153177; CA05481.1;			QY 396 FYNYE----GPAPRBAHNIPHDEFFNSEPNSEIVRNLSCKRPD----OHFKPYLTQDL 444
DR	GO; GO:0004519; F:nucleotide pyrophosphatase activity; IEA.			Db 329 VQSVTPLIAISPPL-----BFSPAEIVAKNNSGLOSGRVNGKHLKVTLKEDL 376
DR	InterPro; IPR01604; Endonuclease activity; IEA.			QY 445 PKRLHYAKNVRIDKWHLFVDQQLAVESVKSNTNCGGNGHGYNEFRSMEAFLAHGSPFK 504
DR	Pfam; PF01223; Endonuclease.			Db 377 PKRLHYSPDSYRAPPGLDGEYKVERORDSNSRNECAHGHDNEYSMRFTIAHGPFA 436
SMART;	SM00477; NUC_C_1.			QY 505 EKTEVEPPENIENVYLNACDLRQPADNNGTHGSLNHL 543
DR	NON_TER_1			Db 437 KGKRVPSSENVQIYLNVTSILDVEGAERNNGSVSFPSVNL 475
SO	SEQUENCE 152 AA; 17449 MW;	E22AD9E08483E932 CRC64;		RESULT 11
QY	724	MWDYFHSSVLIRKHATERNGVNVYSGP1FDNNYDGHFDAPDDBTKHLANTDVPPIPHTYFWV	783	Q723PS PRELIMINARY; PRT; 274 AA.
Db	1	MWDYFHSSVLIRKHATERNGVNVYSGP1FDNNYDGHFDAPDDBTKHLANTDVPPIPHTYFWV	60	Q723PS PRELIMINARY; PRT; 274 AA.
QY	784	LTSCKNKSHTPENCPGMWDLVPLPFIIPRPTNVESCEPGKPKPALWEEFPAHIAVRDVE	843	AC Q723PS; 25, Created)
Db	61	LTSCKNKSHTPENCPGMWDLVPLPFIIPRPTNVESCEPGKPKPALWEEFPAHIAVRDVE	120	AC Q723PS; 25, Last sequence update)
QY	844	LIITGLDFYQDKYQVPSBTIQLKTYLPFETTTI	975	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db	121	LIITGLDFYQDKYQVPSBTIQLKTYLPFETTTI	152	DE Hypothetical protein DKFZP68GP13218.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606;			GN OS Homo sapiens (Human).
Q9FS13	PRELIMINARY;	PRT; 479 AA.		OC OC
AC	Q9FS13_	Created)		RN [1]
DT	01-MAR-2001	(TREMBLrel. 16, Created)		RP SEQUENCE FROM N.A.
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		RC TISSUE=human rectum tumor;
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		RA Bloecher H., Boesch M., Newes H.W., Weil B., Amid C., Osanger A.,
DE	Nucleotide pyrophosphatase-like protein.			RA Fobo G., Han M., Wienmann S.,
GN	SPNPLP1.			RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
OS	Spinacia oleracea (Spinach).			DR BX537510; CAD97789.1; -.
OC	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Spinacia; Spinacia oleracea (Spinach).			KW Hypothetical protein.
SEQUENCE	274 AA;	30960 MW;		SEQNC 5C4AB440D2D759DA CRC64;

Query Match Similarity 15.5%; Score 746; DB 4; Length 274;
 Best Local Similarity 54.3%; Pred. No. 5.3e-55;
 Matches 140; Conservative 37; Mismatches 78; Indels 2; Gaps 2;
 Qy 322 EEDSSSHAGGPVPSARYKALQVVDIAFQMLMEGLKQRNLANCNTILLADHGMQDQTCN 381
 Db 3 EEDSSGHGSPVSEVKALQVRDGNGVGMIDGLKLNLISDHMGQGSCX 62
 Qy 382 KHEYMTDYPFRINFFYMEGPAPRIRAHNTPHDFSENSEEVTNLUSCRSPDQHEFKPVL 441
 Db 63 KYILNKYLGDVKNIKVYGPAPLRSVDPDKYSSFNVEGYTARNISCREPNQHEKPKYL 122
 Qy 442 PDLPLKRLHAYKQVNRIDKWLFDQOWLAVERSNTNCGGGNHGTYNNNEFRMEAFLANG 500
 Db 123 HTPPKRLFEAKDRDRIEPLTFDPOQALANLNSERKYGCSFRGSDNVNSMQLAVFGIG 182
 Qy 501 PSFKEKTEVPEPFNIEYNLMDLLRQAPANGTHGSNLKVPFYEPESHAEEVSKPS 560
 Db 183 PGPKHGTIADTFTNIEYNLMDLLNTPAIPANGTHGSNLKLPVTPKHPREVHLV 242
 Qy 561 VCGFANPLPTESUDCFC 577
 Db 243 QCPFTTRN-PRDNIGSC 258

RESULT 12

Q9SU83 PRELIMINARY; PRT; 496 AA.
 ID Q9SU83; PRELIMINARY; PRT; 496 AA.
 AC Q42974; PRELIMINARY; PRT; 479 AA.
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Nucleotide pyrophosphatase-like protein (EC 3.6.1.9).
 GN T16L1.190 OR At4g29680
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Spermatophyte; Viridiplantae; Embryophyta; Tracheophyta;
 CC Eurosids II; Brassicales; Brassicaceae; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 RN [1] - TAXID=3702;
 RP SEQUENCE FROM N.A.
 RA Bevan K., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,
 RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2] -
 RP SEQUENCE FROM N.A.
 RA SEQUENCE FROM N.A.
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3] -
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL079344; CAB45328.1;
 DR EMBL; AL161575; CAB79726.1; -;
 DR PIR; T09391; T09391.
 DR GO; GO:0009117; F:hydrolyase activity; IEA.
 DR GO; GO:0004551; F:nucleotide diphosphatase activity; IEA.
 DR InterPro; IPR002591; Phosphodiester.
 DR Pfam; PF01663; Phosphodiester; 1.
 KW Hydrolase.
 SQ 496 AA; 54678 MW; 8DC2B346121D732 CRC64;

Query Match Similarity 15.5%; Score 743.5; DB 10; Length 496;
 Best Local Similarity 41.0%; Pred. No. 2e-54;
 Matches 159; Conservative 71; Mismatches 141; Indels 17; Gaps 9;

Qy 157 DLPPVLFMSMDGFRAEYLWDTIMPNKLTKTGIHSKY-NRAMYPIKTEPNTHYITVG 215

Db 105 DKPVVLLISSDGFR - FGQYQFKTKLPSIHLIANGTEAETGLIIPVFPTLTFFNHYSTIVTG 162
 Qy 216 LYPESSHGIIIDNNMYDVNNLNKNFSLSRKQNPNPAWHDGPMWLTAMYQOLKAATYFWPGE 275
 Db 163 LYPAHGIIINHHFVDPETGNVFMASHE -- FEWLGBPLKETVANQGLKAATYFWPGE 219
 Qy 276 VATNSF --PSYMPYGVSPPERERISPLLKLDPLAERPRFTYMFEEPIPSSGIAGG 332
 Db 220 VH-KGSWNCPQGLQONYNGSVPFDRTILSYFDFDPSNEISFMLYFEDPDHQHQVQ 278
 Qy 333 PVASRVIKALQVWDHAFGMLMEGLKQRNLHNCVNILLADHGMQDQTCNKMMEYMTDYPR 392
 Db 279 PDDPDTAEVNNDRLGLIGDEKR1 FEDTMWGDHGPVGTCDKLVLVLDLDPW 338
 Qy 393 INF--FYMVEGPAPRIRAHNPHDFFSNSEEIVRNLSCKRD- -QHFKPVLTDPLPKR 447
 Db 339 IKIPBSWVQYXTPLAIQEPS-GHDAADIVA-KINEGSGKVNGYKLVTKLREDLPSR 396
 Qy 448 LHYANVNRDVKHFLFDQWLNRSKNTNCG-GNGHGNNEFNSMEAFLANGPSEKRT 507
 Db 397 LHYYDSDRIPPLGIVDESFKVEQKSXAKECGGAGHDNAFFSMRTIFIGHGPMFSKGR 456
 Qy 508 EVEPENIEVYNNMCDLRQIOPAENG 535
 Qy 457 KVPSPEVQIYVVISIQLKAPNGS 484

RESULT 13

Q42974 PRELIMINARY; PRT; 479 AA.
 ID Q42974; PRELIMINARY; PRT; 479 AA.
 AC Q42974; PRELIMINARY; PRT; 479 AA.
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Nucleotide pyrophosphatase precursor (EC 3.6.1.9) (OSE4) (Nucleotide pyrophosphatase homolog).
 DE OSE4 OR P0419001.2.
 GN Oryza sativa (Rice).
 OC Bakuryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 RN [1] - TAXID=4510;
 RN SEQUENCE FROM N.A.
 RP STRAIN=TAINUNG 67;
 RC RA Hsing Y.-C., Tao C.-V., Chow T., Hsieh J., Chen Z.-H.,
 RC RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RL RN [2] -
 RN SEQUENCE FROM N.A.
 RP RC STRAIN=CV_1R04;
 RC RA Hsing Y.-I.C., Hsu T.-F., Chen Z.-Y., Chung M.-C., Tsou C.-H.,
 RC RA Hsieh J.-S.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN RT "Characterization of a rice early embryogenesis specific gene OSE4.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3] -
 RP SEQUENCE FROM N.A.
 RC RC STRAIN=CV_N.A.
 RC RA Sasaki T., Matsumoto T., Yamamoto K.;
 RC RA Hsieh J.-S.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR DR U25430; AAA67067.1;
 DR DR AF245483; AA65459.1;
 DR DR AP003244; BAB56086.1;
 DR PIR; T03293; T03293;
 DR DR Gramene; Q42974; -
 DR DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0004551; F:nucleotide diphosphatase activity; IEA.
 DR GO; GO:009117; P:nucleotide metabolism; IEA.
 DR InterPro; IPR02591; Phosphodiester.
 DR Pfam; PF01663; Phosphodiester; 1.
 KW Hydrolase; Signal.

FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	479	NUCLEOTIDE PYROPHOSPHATASE.
SQ	SEQUENCE	479 AA;	52198 MW;	8E209C3DA17B7220 CRC64;
Query Match		15.4%	Score 737.5 ; DB 10 ; Length 479;	
Best Local Similarity		42.0% ; Pred. No. 6.3e-54 ;	Indels 21 ; Gaps 10 ;	
Matches	163 ; Conservative	64 ; Mismatches 140 ;	Indels 21 ; Gaps 10 ;	
Qy	159 PPIVLFPSMDGFRAEYLWTDLMPNFIKLKGTHSKY-MRAMYPTKTFPNHYTIVTGLY	217		
Db	90 PVIILISSDGFRGYQHAAAT--PHIRLIGNTSIAATGLVPIFPLTPNPHYSIATGLY	147		
Qy	218 PESHGIIIDNNMYDVNLNKFNSLSSXONNPWMMGCPMLMTAMYQGLKATAYTWFPGSEVA	277		
Db	148 PESHGIIINYYFDPISDFPMSHSE--PKWNLGPWLWTAADCGIQATAYTWFGEYR	204		
Qy	278 INGSF- PSIY MPYNGSVPPFPEERISTLKLWDLKAERPRFYTMYFEEDPSSGHAGGPV	334		
Db	205 -KGSDWDCPDKYCRHYNSVPPFEEVRDAILGFDLPSDEMPOFQLFLYTFEDDHQHGVGD	263		
Qy	335 SARVIALQVQDHAEGMILEGUKQRNLHNCVNIILLADHGDMDQTYCNKBEYMTDFPRZN	394		
Db	264 DPAITEAVVRIDEMIGRLIAGLEERGVFEDVNVLVGDHMGVTCDDKLYVFLDELAPWK	323		
Qy	395 F--FVNYEGPAPRITAHHNIPHDFFFN--EEITVNLNSCRKPD-QHFPYLPITDLPKR	447		
Db	324 LBEDWVLSMTPLAIR---PPDDMSLSPDVYARMEGLGGKVVEGYRMYLKDLPKR	379		
Qy	448 LHYAKNVRIDKWLHFVDQWNLAVRSKSNTNGGGNHGYNNFRSMEAIFLAHGSPSEKET	507		
Db	380 LYHADSTRPIPPIGLDEEGYKEMVRSKDRNECGGAHGYDNFAFFSRTFTIAHGRFEGGR	439		
Qy	508 EVEPFENIEVYNLMCDLRLIOPAPNNGT 535			
Db	440 VVPSENFEVYVNAIASLNLPEPNNGS 467			
RESULT 14				
ID	Q84WJ3	PRELIMINARY;	PRT;	457 AA.
AC	Q84WJ3;			
DT	01-JUN-2003 (TREMBLrel. 24. Created)			
DT	01-JUN-2003 (TREMBLrel. 24. Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25. Last annotation update)			
DB	At4g29690.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TAXID=3702;			
RN	SEQUENCE FROM N.A.			
RA	Beyan M., Rose M., Hemptel S., Entian K.-D., Bancroft I., Newes H.W., Mayer K.F.X., Schueler C.;			
RA	Mayer K.F.X., Zentcke K., Schueler C.;			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
RN	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RA	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
RN	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	BT003154; AAQ04586; 1;			
GO	GO:0016787; F:hydrolyase activity; IEA.			
GO	GO:0009117; P:nucleotide metabolism; IEA.			
InterPro	IPR002591; Phosphodiester.			
Pfam	Pf01663; Phosphodiester.			
SEQUENCE	457 AA; 51233 MW; 3F5F9DBA9131D0D CRC64;			
SQ	QQSQCPEGFDLPPVLFMSMGFRAYLYTDTMPNINKTGTGHSKX-MRAMYPTKTF 206			
Query Match	14.9% ; Score 713.5 ; DB 10 ; Length 457;			
Best Local Similarity	38.5% ; Pred. No. 6.4e-52;			
Matches	166 ; Conservative	76 ; Mismatches 148 ; Indels 41 ; Gaps 12 ;		

Query Match 14.8%; Score 712.5; DB 1.0; Length 457;
 Best Local Similarity 38.5%; Pred. No. 7.8e-52;
 Matches 166; Conservative 76; Mismatches 148; Index 41; Gaps 12;

Qy 148 QSQQCPCGFDLPPVILFSMDGFRAEVLYTWTLMPNINKLKTG3HSKY-MRAMYPTKTF 206
 Db 44 RRFQPPPKLNKVVLISCDGFREGQFKTET--EPIDLLISRGTEAKTG1IPVPTMTP 101

Qy 207 PHEYTIVTGLYPESHGILIDNNMYDNLNKNESLSSKEONNPAAWWGQQPWNLTAMYQGLKA 266
 Db 102 PHYSIATGGLYPAASHGILIMNKFTDPYSGELEN---RNLAEPKWNLGEPLWVTAVNOGLMA 157

Qy 267 ATYFWPGSEVAINGSF --PSIY -MPNGSYVPEERISTLKWDLPKAERPRFYTMYFE 322

Db 158 ATYFWPG2DVH-KGSWNOPKGCKAPNVSPLEERVTDTINYFDLPREFDMALYFD 216

Qy 323 EPDSSEGHHGGPVSARVITALOVDHAFGMLMEGLKORNLLNCVNILLADIGMDQTYCNK 382

Db 2117 EPIQGHYGPDDPRVTEAVSKDGRIMGRIMGLEKRKVFSDVAVILLDEGMVNTNCDKK 276

Qy 383 MBYMTDYFPRINFFYMEYGPAPRIRAHNIPHDFESFN----- SEEIVRN-- 426

Db 277 VIYIDDIAWDIKI-----PADWICDYS --- PVLAXNPRWGKDVKNPQKNAELVRKME 327

Qy 427 -LSCRK--PDQEFKPYLTDKLRLAYKANRIDKYLFDQMLAVRSKSNTNGGGNH 483

Db 328 ALSSGKVYANGEFIQVYKENLPQLHYSDSRIPLIGMSEGILMKQNRTYVQECGTH 387

Qy 484 GYNNEFRAMEAIFLAHGSFKEKTEVFENTEBVNLMDLLR1QPAANNTHGSLNHLJ 543

Db 368 GYDNMFEMRS1FVGYGRFRRGKIVPSENQVNAVAELIGLRPAPNGSSLFTRSLL 447

Qy 544 KYPFYEPHAE 554

Db 448 -LPRGETSQVE 457

Search completed: July 6, 2004, 13:19:49
 Job time : 52 secs

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Scoring table:	BLOSUM62					
Gapopen:	10.0	Gapext: 0.5				
Searched:	141681 seqs, 52270155 residues					
Total number of hits satisfying chosen parameters:	141681					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0%	Maximum Match 100%				
	Listing First 45 summaries					
Database :	SwissProt_42:					
Pred.	No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
		SUMMARIES				
Result No.	Score	Query	Match	Length	DB ID	Description
1	4804	100.0	875	1	NPP3_HUMAN	014638 h ectonucle
2	3982	82.9	875	1	NPP3_RAT	P97675 r ectonucle
3	2495	52.0	925	1	NPP1_HUMAN	P22413 h ectonucle
4	2424	50.7	906	1	NPP1_MOUSE	P06802 m ectonucle
5	2405	50.1	906	1	NPP1_RAT	Q924C3 r ectonucle
6	2091	43.9	862	1	NPP2_MOUSE	Q9r166 m ectonucle
7	2091.5	43.5	863	1	NPP2_HUMAN	Q13822 h ectonucle
8	2043.5	42.5	885	1	NPP1_RAT	Q84610 r ectonucle
9	2434.5	9.0	742	1	YCR6_YEAST	P23535 saccharomy
10	4124.5	8.6	943	1	YEB6_YEAST	P39997 saccharomy
11	391	6.3	61	1	PPD1_BOVIN	P15396 bos taurus
12	130	2.7	476	1	TNAG_HUMAN	Q9ujw2 homo sapien
13	129	2.7	369	1	PP11_HUMAN	P21128 homo sapien
14	126	2.6	2004	1	YPR73_YERPE	Q8zdj2 Yersinia pe
15	121	2.5	4543	1	LRP1_CHICK	P9f157 Gallus gallus
16	119	2.5	1378	1	WR52_ARATH	Q9fh83 arabidopsis
17	116.5	2.4	758	1	YA93_SCHPO	Q97982 schizosacch
18	115.5	2.4	704	1	SSP1_BOMMO	P20163 bombyx mori
19	114	2.4	1105	1	STC_DROME	P40798 drosophila
20	114	2.4	4544	1	LRP1_HUMAN	Q07954 homo sapien
21	113.5	2.4	368	1	NUGL_HUMAN	Q9y2c4 homo sapien
22	113.5	2.4	1808	1	TENA_CHICK	P10039 Gallus gallus
23	113	2.4	474	1	KLF4_MOUSE	Q60793 mus musculus
24	112.5	2.3	322	1	PN11_SCHPO	Q10480 schizosacch
25	112.5	2.3	854	1	LDLR_CRICKER	P35950 crioceris
26	112	2.3	2352	1	MORC_SCHPO	Q9u14 schizosacch
27	112	2.3	873	1	LDLR_RAT	P25952 rat
28	111	2.3	329	1	NUCL_YEAST	P08466 saccharomy
29	111	2.3	662	1	FAST1_SCHPO	P10675 schizosacch
30	111	2.3	1442	1	DPO3UREA	Q9pb4 ureaplasma
31	110	2.3	1700	1	BAR2_CHIPE	Q03376 chironomus
32	110	2.3	1926	1	LPH_RABIT	P09499 cryptotilagous
33	109.5	2.3	871	1	SUL1_HUMAN	Q8iwu6 homo sapien

ALIGNMENTS

Title:	US-10-005-480A-743	
Perfect score:	4804	
Sequence:	1 MESITLATEQPKVKNTLKK.....QPVSEILQLKTYLPTFTETI	875
Scoring table:	BLOSUM62	
Gapopen:	10.0	Gapext: 0.5

RESULT 1

NPP3_HUMAN	STANDARD;	PRT;	875 AA.
ID NPP3_HUMAN			
AC O14638;			
DT 28-FEB-2003 (Rel. 41, Created)			
DT 28-FEB-2003 (Rel. 41, Last sequence update)			
DT 28-FEB-2003 (Rel. 41, Last annotation update)			
DE Ectonucleotide pyrophosphatase/phosphodiesterase 3 (E-NPP 3)			
DE (Phosphodiesterase I/nucleotide pyrophosphate 3') Phosphodiesterase			
DE I beta) (PD-Ibeta) (CD03C antigen) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotides pyrophosphatase			
DE (EC 3.6.1.9) (NPase)] .			
DB ENPP3 OR PDNP3.			
RN SEQUENCE FROM N.A.			
RP PROSTATE;			
RC TISSUE=Prostate;			
RD MEDLINE=9808833; PubMed=9344666;			
RA Piao J.-H., Goding J.W., Nakamura H., Sano K.;			
RT "Molecular cloning and chromosomal localization of PD-Ibeta (PDNP3), a new member of the human phosphodiesterase I genes.";			
RT RT new member of the human phosphodiesterase I genes.";			
RL Genomics 45:412-415 (1999).			
RN SEQUENCE OF 189-875 FROM N.A.			
RP Wohldmann P., Le T.;			
RA Hou S., Wohldmann P., Le T.;			
RT Genomics 45:412-415 (1999); to the EMBL/GenBank/DDBJ databases.			
CC -I- FUNCTION: Cleaves a variety of phosphodiester and phosphosulfate bonds including deoxynucleotides, nucleotide sugars, and NAD (By similarity).			
CC -I- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.			
CC -I- CATALYTIC ACTIVITY: A dinucleotide + H(2)O = 2 mononucleotide.			
CC -I- SUBCELLULAR LOCATION: Type II membrane protein.			
CC -I- SUBCELLULAR LOCATION: Contains 2 somatotropin type domains.			
CC -I- DATABASE: NAME-PROW NOTE-PROW 1-7-49(2000);			
CC WWW="http://www.ncbi.nlm.nih.gov/prog/guide/575821061_g.htm".			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC DR EMBL; AF05632; AAC5181; ;			
CC DR EMBL; AC00587; AA0519; ;			
CC DR Genev.; HGNC:3358; ENPP3.			
CC DR NM: 60282;			
CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.			
CC DR GO; GO:004551; Fructolide diphosphatase activity; TAS.			
CC DR GO; GO:004528; F:phosphodiesterase I activity; TAS.			

GO: GO_0006796; P: phosphate metabolism; TAS.				
DR InterPro; IPR01604; Endonuclease.				
DR InterPro; IPR002391; Phosphodiester.				
DR InterPro; IPR001212; Somatomedin_B.				
PFam; PF01243; Endonuclease;				
PFam; PF01033; Somatomedin_B; 1.				
DR SMART; SM00477; NUC; 1.				
SMART; SM00201; SO; 2.				
PROSITE; PS00524; SOMATOMEDIN_B; 2.				
Glycoprotein; Transmembrane; Repeat; Signal-anchor; Hydrolase;				
KW				
KW				
FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 12 30 SIGNAL ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).				
FT DOMAIN 31 875 EXTRACELLULAR (POTENTIAL).				
FT DOMAIN 50 93 SOMATOMEDIN-B LIKE 1.				
FT DOMAIN 94 138 SOMATOMEDIN-B LIKE 2.				
FT DOMAIN 140 510 PHOSPHODIESTERASE.				
FT DOMAIN 605 875 NUCLEASE.				
FT ACT SITE 205 BY SIMILARITY.				
FT SITE 78 80 CELL ATTACHMENT SITE (POTENTIAL).				
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 687 687 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 699 699 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT CARBOHYD 789 789 N-LINKED (GLCNAC. . .) (POTENTIAL).				
SQ SEQUENCE 875 AA; 100096 MW; 329CF41667497BC4 CRC64; Score 4804; DB: 1; Length 875; Best Local Similarity 100.0%; Score 100.0%; Pred. No: 0; Indels 0; Gaps 0; Matches 875; Conservative 0; Mismatches 0; Gaps 0;				
Qy 1 NESTLTIAEQIVKNTLTKYKIACTIVLLAVLIVMSLGLIGLGLRKLKMQGSCRKCKCFD 60				
Db 1 NESTLTIAEQIVKNTLTKYKIACTIVLLAVLIVMSLGLIGLGLRKLKMQGSCRKCKCFD 60				
Qy 61 ASFRGLENCRDVACKDRGDCWDFFDTCTYESTR1WMCNFKRCGETRLASLCSCSDDCI 120				
Pb 61 ASFRGLENCRDVACKDRGDCWDFFDTCTYESTR1WMCNFKRCGETRLASLCSCSDDCI 120				
Qy 121 QKRDCCADYKSVCQGETSWILEENCDTAQQSOCPEGFDLPVILFSDMDGEAEVLYTWTDL 180				
Db 121 QKRDCCADYKSVCQGETSWILEENCDTAQQSOCPEGFDLPVILFSDMDGEAEVLYTWTDL 180				
Qy 181 MENTNIKLTGHSKYNRAAMPYKTPPNHHTIVTGYPEHGIDDNMYDVLNLINKNFSLS 240				
Db 181 MENTNIKLTGHSKYNRAAMPYKTPKTFPNHHTIVTGYPEHGIDDNMYDVLNLINKNFSLS 240				
Qy 241 SKEQNNPAAWHGQPMLTAMYQLKATYFWPGSEVAINGSFPSYMPNGSYFEEIRLS 300				
Db 241 SKEQNNPAAWHGQPMLTAMYQLKATYFWPGSEVAINGSFPSYMPNGSYFEEIRLS 300				
Qy 301 TLLKWLDPKAERPRFTYMPPEEPDSGHAGGPVSARVIALQVVDHAFLMGLKORN 360				
Db 301 TLLKWLDPKAERPRFTYMPPEEPDSGHAGGPVSARVIALQVVDHAFLMGLKORN 360				
Qy 361 LHNCVNTILLADHGMMQTYCNGMENMTDYPRIINFYMEGPAIRAINIPDFFSENS 420				
Db 361 LHNCVNTILLADHGMMQTYCNGMENMTDYPRIINFYMEGPAIRAINIPDFFSENS 420				
Qy 421 EIVRNLSCKRPDOHKPKPVLTDPLKRLHYAKNRIDKVKLYDQOILARSKSNTNGCG 480				
Db 421 EIVRNLSCKRPDOHKPKPVLTDPLKRLHYAKNRIDKVKLYDQOILARSKSNTNGCG 480				
Qy 481 GNGHYNNEFRSMEAIFIAGHSFSKETEVEPPENLEVINMCDLIRIOPAPNNGTHGSIN 540				
Db 481 GNGHYNNEFRSMEAIFIAGHSFSKETEVEPPENLEVINMCDLIRIOPAPNNGTHGSIN 540				

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VARIANT	124	124	K -> E.
VARIANT	201	201	N -> V.
VARIANT	596	597	SG -> NR.
CONFLICT	111	111	A -> T (IN REF. 3).
CONFLICT	273	273	P -> L (IN REF. 1).
CONFLICT	475	476	SS -> VP (IN REF. 3).
CONFLICT	514	514	X -> VP (IN DEF. 2).

1 CONFLICT 814 814 -> NF (\IN REC. 3);
 SEQUENCE 875 AA; 99071 MW; 4205F263E8A933EA CRC64;
 SQ

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	Query	Document	Score	Pred	Label	Length
Best local similarity	81 3%	locally	53.61	Pred	96	277
	81 3%	locally	53.61	Pred	96	277
	81 3%	locally	53.61	Pred	96	277
	81 3%	locally	53.61	Pred	96	277

Matches 712; Conservative 77; Missmatches 85; Indels 2; Gaps 2

1 MESTLTLATEOPVKRQNTKCYRIACIVALL
1 GIGGLGLRKLERO-GSSCRKCF
59

לְבָנָה מִשְׁׂרָבָה וְמִשְׁׂרָבָה כְּבָנָה
לְבָנָה מִשְׁׂרָבָה וְמִשְׁׂרָבָה כְּבָנָה

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60 DASFRGLENCRDVACKDRCGCCWDFEDTCVESTRINMCMNKFRCGETRLEASLCSDDC 119
61 2Y

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61 DSSERGLEGCRCDSGCTDRGDCWDFEDICVRSIQIWICNSFRQGBIRLEHALCSADD 120

120 LOKEDCCADYKSVCOGETSWLEENCDDAQOSOCPEGFDLPPVILFSDMGFRABLYTWTDT 179
DOV

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121 LQRKDCCDYKAVCQGEVWPWTEACASSQEPQQCPFGDOPPVILFMSDGFRAYLOTWST 180

QY	180	LMPNNINKLTCGTHSKYKAMAMPTRTPNHYTIVGLYPSESRGIIDNNMVDVNKNFSL	239
Db	181	LLPNINKLXTCGLISKYMAMAMPTRTPNHYTIVGLYPSESRGIIDNNMVDVNKNFSL	240
QY	240	SSKEENNPAWHGQPMMLTAMYQGLKAATFWPGSEVAINTSFPSIYMPYNGSVPPFEERI	299
Db	241	SSVEENPAWNSQGQITLAMYQGLKAASYWPGDVAVGSFNPVYRNVSNSVPEESRI	300
QY	300	STILKWIDLPKAERPRFTMYFEEDPSCHAGGPYSARVIALQVYDHAFGMMLMEGSIKQR	359
Db	301	ATLQWLDPKAERSFTYTYEEEDSAAGHSKSPSAGVIALQVYDDAFAFGMMLMEGIKQR	360
QY	360	NLHNQCVNILLADHGMQTYCNRQEYMTDYPRINFFYMEGPARIRAINPHDFESN	419
Db	361	NLHNQCVNILLADHGMQTYCDRVSYMTDYEPEIN-FYMYQGPAPRTRTNTPQDFETEN	419
QY	420	SEEITVRNLSCRKDHPDKFKPVLTPDLPKRLIAKVNTRIDKHLFDQCLWLA VRKSNTNCG	479
Db	420	SEEITVLDLSRKSDHFKPKVLTPDLPKRLIAKVNTRIDKHLMDRQLAVRNKGSSNCE	479
QY	480	GGNHGYNNEFRSMEAIFLAHGSPSKERTEVFENIEVNLCDLIRIOPAPNNGTHGSL	539
Db	480	GGTHGYNNEFRSMEAIFLAHGSPSKERTEVFENIEVNLCDLIRIOPAPNNGSHGSL	539
QY	540	NHLKVPFPYPSHAEVSKSVCVGGANPLTESLDCFCPHQNSTQLECYQNMNLJQEE	599
Db	540	NHLKVPFPYPSHAEVSKSVCVGGANPLTESLDCFCPHQNSTQLECYQNMNLJQEE	599
QY	600	ITATVKNLPGGRPRVTLQKRNVDHCLLYHREYVSGFCKAMRNPWMSSYTVPQLGDTSLPP	659
Db	600	VSATEKTNLPFGRPRTVIQKNDKDHCLLYHREYVSGFCKAMRNPWMSSYTVPQLGDTSLPP	659
QY	660	TVPDCIRADYRVPPSESQKCSFYLADKNTHTGFLYBPASNRTSDSOYDALITSNLVNYE	719
Db	660	TVPDCIRADYRVDPSESQKCSFYLADKNTHTGFLYBPASNRTSDSOYDALITSNLVNYE	719
QY	720	EFRKWDYEFISVLLKHAERNGVNVSGPFLDYNNDGHFDAPDEITKHLANTDVPIPTH	779
Db	720	EFRKWDYEFISVLLKHAERNGVNVSGPFLDYNNDGHFDAPDEITNVAFTDVPIPTH	779
QY	780	YFVUTLTSCKNSHTPENCPGMWDLPLIPHRPTNYESCPEGKPEALWEERTFAHTARV	839
Db	780	YFVUTLTSCKNSHTPENCPGMWDLPLIPHRPTNYESCPEGKPEALWEERTFAHTARV	839
QY	840	RDVELLTGLDPFQDVKQPVSETLQLKTYLPFTETI	875
Db	840	RDVELLTGLDPFQDVKQPVSETLQLKTYLPFTETI	875
RESULT 3			
NPP1_HUMAN			
ID	NP_00113	STANDARD; PRT; 925 AA.	
AC	P22413; Q9UPZ3; Q9UPIP6; Q9UP61; Q916K3;		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Bctonucleotide Pyrophosphatase/phosphodiesterase 1 (B-NPP 1)		
DE	(Phosphodiesterase I/nucleotide Pyrophosphatase 1) (Plasma-cell membrane glycoprotein PC-1) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.5.6.1.9) (NPPase 1)].		
DE	ENPP1 OR PDNP1 OR PCL OR NPPS.		
OS	Homo sapiens (Human).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	Medline=91009202; PubMed=2211644;		
RA	Buckley M.F., Loveland K.A., McKinstry W.J., Goding J.W.;		
RT	"plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule, amino acid sequence, and chromosomal location." J. Biol. Chem. 265:17506-17511(1990).		

```

RESULT 3
NPP1_HUMAN
ID P224
AC 01-AA
DT 28-F
DT 28-F
DT 28-F
DE Ecto
DE (Pho)
DE memb
DE (EC
DE DE
GN ENPP
OS CS
OC Buka
OC Mamm
OX NCBI
RN [1]
RP SEQU
RP MEDU
RX Buck
RA "Pla
RT RT
RT RT
RL RL
RN RN

```

RP SEQUENCE FROM N.A.
 RX MEDLINE=92246539; PubMed=1315502;
 RA Funakoshi T., Kato H., Horie K., Yano T., Hori Y., Kobayashi H.,
 RA Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,
 RA Yamashin I.;
 RT "Molecular cloning of cDNAs for human fibroblast nucleotide
 pyrophosphatase";
 RL Arch. Biochem. Biophys. 295:180-187(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Bozzali M., Pizzutti A., Trischitta E.;
 RT "Genomic structure of the human PC1 gene,";
 RL Submitted (APR-1999) to the EMBL/GenBank/DDJB databases.
 RN [4]
 RP SEQUENCE OF 81-925 FROM N.A.
 RA Peck A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDJB databases.
 RN [5]
 RP SEQUENCE OF 145-185 FROM N.A., AND VARIANT GIN-173.
 RX MEDLINE=99408501; PubMed=10480624;
 RA Pizzutti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,
 RA Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,
 RA Tassi V., Trischitta V.;
 RT "A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding
 region is strongly associated with insulin resistance.";
 RT Diabetes 48:1881-1884 (1999).
 RL [6]
 RP CHARACTERIZATION.
 RX MEDLINE=95054801; PubMed=8001561;
 RA Belli S.I., Goding J.W.;
 RT "Biochemical characterization of human PC-1, an enzyme possessing
 alkaline phosphodiesterase I and nucleotide pyrophosphatase
 activities";
 RT Eur. J. Biochem. 226:433-443 (1994).
 RN [7]
 RP ACTIVE SITE.
 RX MEDLINE=95235270; PubMed=7337162;
 RA Mercuri P.A., Sall A., Goding J.W.;
 RT "Autophosphodiesterase I (alkaline phosphodiesterase I/nucleotide
 pyrophosphatase) and analysis of the active site.";
 RT Pyrophosphatase and analysis of the active site.";
 RL Eur. J. Biochem. 228:669-676 (1995).
 RN [8]
 RP VARIANTS OPLL PRO-91 AND PHE-287, AND VARIANTS GIN-173; HIS-268 AND
 PRO-779.
 RX MEDLINE=99381851; PubMed=10453738;
 RA Nakamura I., Ikegawa S., Okuda S., Koshizuka Y.,
 RA Kawaguchi H., Nakamura K., Koyama T., Goto S., Toguchida J.,
 RA Matsushita M., Ochi T., Takeo K., Nakamura Y.;
 RT "Association of the human NPPS gene with ossification of the posterior
 longitudinal ligament of the spine (OPLL)." ;
 RT Human Genet. 104:492-497 (1999).
 CC -!- FUNCTION: Has a broad specificity and cleaves a variety of
 substrates, including phosphodiester bonds of nucleotides and
 nucleotide sugars and pyrophosphate bonds of nucleotides and
 nucleotide sugars. Can hydrolyze nucleoside 5'-triphosphates such
 as ATP, GTP, CTP, UTP and UTP from their corresponding
 monophosphates with release of pyrophosphate. Can hydrolyze
 diadenosine polyphosphates and 3',5'-cAMP to AMP. It may play a
 role in the regulation of pyrophosphate production, the regulation
 of the availability of nucleotide sugars in the endoplasmic
 reticulum and Golgi, and the regulation of purinergic signaling.
 CC -!- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides
 successively from the 3'-hydroxy termini of 3'-hydroxy-terminated
 oligo-nucleotides.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
 OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
 OF THE KIDNEY, CHONDRYCYTES, AND EPIDIDYMIS.
 CC -!- PTM: Autophosphorylated as part of the catalytic cycle of
 phosphodiester/pyrophosphatase activity.
 CC -!- PTM: N-glycosylated.

and analysis of expression.";

Proc. Natl. Acad. Sci. U.S.A. 82:8619-8623 (1985).

[5] RN

PARTIAL SEQUENCE.

MEDLINE=85056299; PubMed=3917281;

RT Stearne P.A., van Driel T.R., Grego B., Simpson R.J., Godding J.W.;

"The murine plasma cell antigen PC-1: purification and partial amino acid sequence.";

J. Immunol. 134:443-448 (1985).

[6] RN

DISEASE.

RX MEDLINE=98324779; PubMed=9662402;

RA Okawa A., Nakamura I., Goto S., Moriya H., Nakamura Y., Ikegawa S.; "Mutation in Nppa in a mouse model of ossification of the posterior longitudinal ligament of the spine.";

RT Nat. Genet. 19:271-273 (1998).

-!- FUNCTION: Has a broad specificity and cleaves a variety of substrates, including phosphodiester bonds of nucleotides and nucleotide sugars and pyrophosphate bonds of nucleotides and nucleotide sugars. Can hydrolyze nucleoside 5' triphosphates such as ATP, GTP, CTP, TTP and UTP to their corresponding monophosphates, with release of pyrophosphate. Can hydrolyze diadenosine polyphosphates and 3', 5'-cAMP to AMP. It may play a role in the regulation of pyrophosphate production, the regulation of the availability of nucleotide sugars in the endoplasmic reticulum and Golgi, and the regulation of purinergic signaling (By similarity).

-!- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.

CC -!- CATALYTIC ACTIVITY: A dinucleotide + H₂O = 2 mononucleotide.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named 1isoforms=2;

Name=1; IsoId=P06802-1; Sequence-Displayed;

CC -!- ISOID= P06802-2; Sequence=VSP_006748;

CC -!- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF ANTI-BODY-SECRETING CELLS.

CC -!- PTM: Autophosphorylated as part of the catalytic cycle of phosphodiester/pyrophosphatase activity (By similarity).

CC -!- PTM: The N-terminus is blocked.

CC -!- DISEASE: Defects in ENPP1 are the cause of the tiptoe walking (ttw) phenotype. Ttw mice exhibit ossification of the spinal ligaments.

CC -!- SIMILARITY: Contains 2 somatomedin-B type domains.

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CC EMBL: J02700; AAA38893; 2;

DR DR: M12852; AAA38892; 1; -;

DR DR: PIR: A27410; A27410; -;

DR DR: MGI: 7370; Enzyme;

DR DR: GO:0001501; P:skeleral development; IMP.

DR DR: InterPro: IPR01605; Endonuclease.

DR DR: IPR00259; Phosphodiester.

DR DR: InterPro: IPR01212; Somatomedin_B.

DR DR: Pfam: PF01223; Endonuclease; 1.

DR DR: Pfam: PF01663; Phosphodiester; 1.

DR DR: Pfam: PF01033; Somatomedin_B; 2.

DR DR: PRINTS: PR00022; SOMATOMEDIN_B.

DR DR: SMART: SM00477; NUC; 1.

DR DR: PROSITE: PS00524; SOMATOMEDIN_B; 2.

DR DR: Glycoprotein; Transmembrane;

kw Repeat; Signal-anchor; Hydrolase;

KW Multifunctional enzyme; Polymorphism; Phosphorylation;

KW Alternative splicing.

FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 59 79 SIGNAL ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).

FT DOMAIN 80 906 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 86 126 SOMATOMEDIN_B_LIKE_1.

FT DOMAIN 127 170 SOMATOMEDIN_B_LIKE_2.

FT DOMAIN 173 573 PHOSPHODIESTERASE.

FT DOMAIN 635 906 NUCLEASE.

FT ACT SITE 238 238 BY SIMILARITY.

FT CARBOHYD 161 161 (POTENTIAL).

FT CARBOHYD 267 267 N-LINKED (GLCNAC . . .) (POTENTIAL).

FT CARBOHYD 323 323 N-LINKED (GLCNAC . . .) (POTENTIAL).

FT CARBOHYD 459 459 N-LINKED (GLCNAC . . .) (POTENTIAL).

FT CARBOHYD 567 567 N-LINKED (GLCNAC . . .) (POTENTIAL).

FT CARBOHYD 624 624 N-LINKED (GLCNAC . . .) (POTENTIAL).

FT VARSPLIC 630 630 Missing (in isoform 1).

FT FTID=SP_006748 /

FT VARIANT 651 651 H > R (IN ENPP1_B).

FT VARIANT 680 680 S > R (IN ENPP1_B).

SQ SEQUENCE 906 AA; 103175 MW; 06845B0D0F24D CRC64;

Query Match 50.7%; Score 2434; DB 1; Length 906;

Best Local Similarity 51.0%; Pred. No. 1.6e-16; Matches 447; Conservative 152; Mismatches 250; Indels 28; Gaps 9;

Qy 10 EQPVKK-----NLLKRYKIACTCIVLLAVLIVMSLGIGIGLURKLEKGSCRKCF 59

Db 39 BEPLEKAERARPARKDPY---YKVLYLGLPKSCAVERKSKGKRCF 95

Qy 60 DAFERGLENCRCDVACDRGDCCWDFFDTCESTRIWMCNFRCGEHTREASLCSCDDC 119

Db 96 ERTF--SNCRDAACTSLGNCLDQETCYEPHTIWTCNKFRGEGKRLSRFVCSCADD 152

Qy 120 LOKRDCCADYKSVCOGETSWLLEENCDAQOQSQCPEGFDLPEVILFPEGLDGFRAEVLTYWTD 179

Db 153 KTHNDCCINYYVQCDIKSVWEETCSIDTPCPCPAFSEPTLFLSDLGFAEYHTWG 212

Qy 180 LMPNINKLKTGJHSKMRVAMYPTKTFPNHYTTVGLYPBSHGLIDNNNNYDVNLKNFSL 239

Db 213 LIPVISLKLNCCTYTKMRMPTKTFPNHYTTVGLYPBSHGLIDNNNNYDVNLKNFSL 239

Qy 240 SSKEQNPNPAWHGQPMWLTAMYQGLKATAYFWPGSEVATNSPFSIYMPYNGSUPPERI 299

Db 273 KSKEKTPFLWKQGPWTANHQEVTSKGTFWPGSDVEITGILPDLYKYGTSVFEIERI 332

Qy 300 STLLKWDLPLKAERPREYTMVFEEDPSGHAGGPYSARVKIALQVVDHAFAFGMLMEGLKQR 359

Db 333 LAVLENQLPSHERPFIFTYLYEEPDSSGISHGPYSSEVIKALQVDRLVGMLMDGLKL 392

Qy 360 NHNCVNTILLADHGMDQTYCNGKMYMTDFPRINFFYMEYGPAPRIRAHNIHDFFSPN 419

Db 393 GLDKCLNLLLISDHGMEQGSCKKYYTLYNKXGLDYNVRCVYGPALARLPDVTPEYSSN 452

Qy 420 SEEIVNLSCSKEPKDOPFKPYLTPDLPKRLHYAKNVRIDKVKHFYDQOW-LAVRSKSNTNC 478

Db 453 YEALAKNLSCREPNOFRPLKPLFLKPLRHLFAKSRIEPTFLYDQPQWQJALNPSSRYC 512

Qy 479 GGGNHGYNNBRSMAPAIFLAHGSPSKKEKTEVEPPENIETYVNLMCDLRLIQAPANGTIGS 538

Db 513 GSGFHSDNLTSNMQALFIGGPATKQHGAVIDSFINNEYNLMDLGLGIAPANGTIGS 572

Qy 539 LNHLKVPFYEPRSHAEVSFKSVCGLPMLPTESLDCCFCPHLNISTQLEBVQNMLNLQE 598

Db 573 LNHLKRPYINSPHKPEGFLSQC---PLKSTSNLDGCTCDPWLVPKDFEXOLNLTE 628

Qy 599 EITATVKVNLPGFRPLQKVNDHLLYERVYSGFGKAMRMWSSSTVPOGLDTSPDLP 658

Db 629 DVDDIYHMTVYGRPRILLKOHHVCLLQQQFLTGYSLSDIMPWASYTF--LRNDQFSR 686

Qy 659 PTVPDLTRADVRVPPSESQCSFYLADEKNTIHGFYLPASNRTSDSQY-DALITSNLVYM 717

b	b	b	b	b	b	b	b
687	DDFSNCLYODRILPSPVHEKCSYYKNSKLSYGFLLTPRNLRVSHIYEALLTNSIVPM	746					
718	YEEFRKWDYEHFVSLLIKHATERNGVNVSQPIFDNYDGHFDAPPDEITKH--LANTDV	774					
747	: : : : : : : : : : : : : : : : : :						
747	YQSFQVWHLDTLQRYAERNGVNVSQPVFDPYDGRYDSLEILKQNSVRQSQEI	806					
775	PIPTHYFVVLTSCKNSHTPENCPGWLVLBFIIPIHRPTNYESCPGKPEALWVEERFTA	834					
807	LIPTHFFVLTSCQDSETPLECSA-LESSAVILPDRPDNIESCHGKRESSWIEBLTL	865					
835	HIAKYDVEILTGDFYQDKYQPVSEBLQLKTYLPPTF	871					
866	HRARTTDVEELTGLSFVQDROESSEELLRLKTHLPIF	902					

RESULT 5						
PPI	RAT	STANDARD;	PRT;	906 AA.		
D	NP_41_RAT					
C	Q924C3; Q91XQ3; Q92058;					
T	28-FBB-2003 (Rel. 41, Created)					
T	28-FBB-2003 (Rel. 41, Last sequence update)					
T	28-FBB-2003 (Rel. 41, Last annotation update)					
E	Ectonucleotide Pyrophosphatase/Phosphodiesterase 1 (E-NPP 1)					
E	(Phosphodiesterase 1/nucleotide pyrophosphatase 1) (Plasma-cell membrane glycoprotein PC-1) [Includes: Alkaline phosphodiesterase 1 (EC 3.1.4.1); Nucleolar pyrophosphatase (EC 3.6.1.9); (NPPases)].					
B	ENPP1 OR PDNP1 OR PCL OR NPPS.					
B	Rattus norvegicus (Rat).					
S	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
C	[1] N					
C	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.					
C	STRAIN=Lewis, Louvain, and Wistar;					
C	MEDLINE=22117315; PubMed=12121276;					
A	Banakh I., Sali A., Dubrjevic V., Grobien B., Siegers H., Goding J.W., "Structural basis of allosteric regulation of ecto-nucleotide pyrophosphatase/phosphodiesterase (plasma cell membrane glycoprotein PC-1) in the mouse and rat, and analysis of allele-specific					
X						
X						
P						
C						
C						
A						
A						
T						
T						

Burk, J. Immunoprotect. 29: 307-313 (2002).
-1-
- Enzymatic activities:
- - Has a broad specificity and cleaves a variety of
- substrates, including phosphodiester bonds of nucleotides and
- nucleotide sugars and pyrophosphate bonds of nucleotides and
- nucleotide sugars. Can hydrolyze nucleoside 5'-triphosphates such
as ATP, GTP, CTP, TTP and UTP to their corresponding
monophosphates with release of pyrophosphate. Can hydrolyze
diadenosine polyphosphates and 3', 5'-cAMP to AMP. It may play a
role in the regulation of pyrophosphate production. The regulation
of the availability of nucleotide sugars in the endoplasmic
reticulum may be controlled by this enzyme.

- |- SUBCELLULAR LOCATION: Type II membrane protein.
- |- ALTERNATIVE PRODUCTS:
- |- Event-Alternative splicing; Named isoforms=2;
- |- CATALYTIC ACTIVITY: A dinucleotide + H₂O = 2 mononucleotide
- |- SUBUNIT: Homodimer; By similarity.
- |- SUBUNIT: Monomer; By similarity.
- |- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligonucleotides.
- |- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligonucleotides.
- |- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligonucleotides.
- |- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligonucleotides.

Name=z; Name=Q924C3-1; Sequence=Displayed;
Name=z; Name=Q924C3-2; Sequence=VSP_006749;
-!- PTM: Auto phosphorylated as part of the catalytic cycle of
phosphodiesterase/pyrophosphatase activity (By similarity).
-!- SIMILARITY: Contains 2 soncemedin-B type domains.

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modified and this creation is not commercialized by, and for commercial
purposes.

QY	3.03 LKWLIDLPAERPRFETYMFPEPDSSGHAGGPPSARVIALQVVDHAFGMMEGLKQRLNLH 362 33.6 LEWILQLPSYERPHFTYLYEBPDSIGHSHOPSSSEVIALQVKDVEIVGMLMDGLDGLD 395
QY	36.3 NCVNILLADHGMDTYCNMETYTDYFRPRINFFYMEGAPRIRAHNIPHDFFSFNSEE 422
Db	3.96 KCLNLJLISDHGMCGSCKVYVINKYLGDVNTVTVYGPAAIRLPTVEFETYFSNYEA 455
QY	4.2.3 IVRNLSKRCPDQHEFKPYLTPLDKPLRHLHYAKNRVDRKVLFDQDN-LAVERSKSNTNCGGG 481
Db	4.56 LAKNLSCRETQNHRPFLRPLKFLRHLFAKNDRLEPLTFLDPOQVQLNPSERTYQSGG 515
QY	4.82 NHGTYNEFRSMEAIFIANGPSFEKETEVEPFENIEVYNLMCDLRLIQPAPNNNGHGSLNH 541
Db	5.1.6 PRGSDNLNSNQMLAFIGYGAFKHGAEVDSFENIEVYNLMCDLGLIAPPNNEHGSLNH 575
QY	54.2 LIKVPYFPEBFAEVSKESVCGFAMPPLPESLDFCPHLQNSTQLEQVNQMLNLITQBETT 601
Db	57.6 LIKRPPIYTPSHPKGEESFLSQC ---PIKSVSDDLGCTCOPSIIMFKEQNLITDAVE 631
QY	60.2 ATVKVNLPFLGPRVYLQRNVDHCILLYREVSGFGRAMMPMWSSYTVPOLGDTSPLRPTV 661
Db	63.2 DVYSMTVPGNRPNLQKHRVCLLHQOQLFTGYSLLMLPLWTSYF - LSNDOFSTDDF 689
QY	66.2 PDCLRADYRVPPSESQCSFYLADKRNITHGFLYPPASNRTSDQY - DALITSNLYVPMYEE 720
Db	69.0 SNQLYDQIRIPLSPMHCYSKTSKUSYGLTPPLRNVRVSQIYSEALLTSNLYVPMYQS 74.9
QY	72.1 FRKNDWYFHSSVLLIKHATERGVNVNSGPIFYDNYDGHFDAPD - ETKHLANTDVPIP 777
Db	75.0 FQVIWQYIHDVTIIRRVAERGNVNSVSSPFEDYGRYDSSSLKQNTVRQSQNLIP 809
QY	77.8 THYFVILTSCKNKSHTPENCPGMWLDVLBPFLIIPHRPTNVECPKGKEALWVEERFTAHIA 837
Db	81.0 THFFIVLTSCKQLESPLKCTA-LESSAFLPLRPDNTESCTHKGQESAWBELLALHRA 868
QY	83.8 RYRDVVELTGDFYQDKVQPVSEBILQKTYLPTF 871
Db	86.9 RYTDVVELTGFSYQDQESTSELLRKTHLPIF 902
RESULT 6	
NPP2_MOUSE	SEQUENCE FROM N.A.
AC	STRAIN=C57BL/6;
ID	NP_00116; Q99LG9;
PR	STANDARD; PRT; 862 AA.
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Ectonucleotide pyrophosphatase/phosphodiesterase 2 (E-NPP 2)
DE	(Phosphodiesterase I/nucleotide pyrophophosphate 2) (Phosphodiesterase I (PD-Ialpha)) (PD-Ialpha) [Includes: Alkaline phosphodiesterase 1 (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) (NPPase)].
DE	ENPP2 OR NPPS2
DN	Mus musculus (Mouse)
OS	Mus musculus (Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBITaxonID=10090;
OC	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE:22383257; PubMed=12477932;
RC	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., [2]
RX	Piao J.-H., Matsuda Y., Nakamura H., Sano K.; Assignment of Pdpn2, the gene encoding phosphodiesterase I/nucleotide pyrophophatase 2, to mouse Chromosome 15D2."; Cytogenet. Cell Genet. 87:172-174(1999).
RX	SEQUENCE FROM N.A.
RX	MEDLINE:10169177; PubMed=10702660;
RA	Piao J.-H., Matsuda Y., Nakamura H., Sano K.; Assignment of Pdpn2, the gene encoding phosphodiesterase I/nucleotide pyrophophatase 2, to mouse Chromosome 15D2.";
RA	Cytogenet. Cell Genet. 87:172-174(1999).
RX	SEQUENCE FROM N.A.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., [2]
RX	SEQUENCE FROM N.A.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., [2]

RA	Diatatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Caillavent T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshikuni S., Garninci P., Prange C., Raha S.S., Locqueletto N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Ganatrae P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalton D.K., Muzny D.M., Soederberg E.J., Liu X., Gibbs R.A., Fahey J., Hellon E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyniawski M.I., Smialius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences., Proc. Natl. Acad. Sci. U.S.A. 99:16899-16905 (2002).	
CC	-!- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.	
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein.	
CC	-!- SIMILARITY: Contains 2 somatomedin-B type domains.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	DR ENSEMBL; AF123512; AAD46410; 1; DR ENSEMBL; BC003264; AAH03264; 1; DR NCBI; NGI:13213190; Enpp2. DR InterPro; IPR001604; Endonuclease. DR InterPro; IPR002291; Phosphodiester. DR InterPro; IPR001211; Somatomedin_B. DR Pfam; PF01223; Endonuclease_1. DR Pfam; PF01663; Phosphodiester_1. DR Pfam; PF01033; Somatomedin_B; 2. DR SMART; SM00472; SOMATOMEDIN_B. DR SMART; SM00201; SO; 2. DR PROSITE; PS00524; SOMATOMEDIN_B; 2. KW Glycoprotein; Transmembrane; Repeat; Multifunctional enzyme. FT TRANSMEM 1 11 CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) BY SIMILARITY. FT SITE 12 30 EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN 3 1 862 SCMATOMEDIN B LIKE 1. DOMAIN 54 97 SCMATOMEDIN B LIKE 2. DOMAIN 98 142 DOMAIN 144 501 DOMAIN 597 862 DOMAIN 597 209 DOMAIN 126 128 DOMAIN 53 53 DOMAIN 410 410 DOMAIN 524 524 DOMAIN 806 806 DOMAIN 517 517 DOMAIN 550 550 DOMAIN 573 573 DOMAIN 743 743	
FT	ACT SITE SITE CARBOHYD 53 CARBOHYD 410 CARBOHYD 524 CARBOHYD 806 CARBOHYD 517 CARBOHYD 550 CARBOHYD 573 CARBOHYD 743	
FT	FT CONFLICT 573 FT CONFLICT 573 FT CONFLICT 573 FT CONFLICT 573	
SO	SECRETION 573	

QY 71 CDVACKDRGDCMDFEDTCVSTRIMCNKFRGETEASILCSDDCLOKKCCADYK 130
D 75 CDNLCKSYSSCCCHDFDELCIKTARGWEETKDRGEVENEEVACHCSECDLSRGDCCTNYQ 134

QY 131 SVCGCETSMILEENCDTAQOSQCPEGFDIPVIFSMODGRAYFLYWTDMNPINKLKC 190
D 135 VVCKGEHSHWDDCEBIRVEPCPAGEVAPPLIVFVPPGLIISVGRASYKGSKMPNIELRSC 194

QY 191 GIHSKYMRAAMYPTKTFPPIHYTIVTGLYDESHGLIDNNMYDNLNKFLSSEEQNPAWW 250
D 195 GTHAYMRPYPPTKTFPPIHYTIVTGLYDESHGLIDNNMYDNLNKFLSSEEQNPAWW 254

QY 251 HQOPHMWLTAMYQGKAAATFWPGSEBAVINGSSEPSIIMYNGSVPFERISSLKWLDPK 310
D 255 GGQPWLWTTAKQGYRAGIFW-----SVSPHERRLLTQLWLSLPD 296

QY 311 AERPFTYMFEEBDPSGGAGGGSARVTKALOYDIAFGMMEGALIKORNHNCTNILL 370
D 297 NERPSVAFYFSEQDPDSGHKYGPGPENTNPLREIDTKVGQLMDGKQLKHLRCVNIVFV 356

QY 371 ADHGMDQTYCNKMBMMDYDFPRINFFMYVEGAPRITAHTIPDFFESNSDEIVENLSCR 430
D 357 GDHGMEDVTCDTEFLSLNLTNVIDITVPGTGLGRIP-KTBNN-NDYDPKAIIANLICK 414

QY 431 KPDQHFKPKYLTPDLPKRHYAKNRYDVKHFLDQON-----LAYRSKSNTNC-GGNH 483
D 415 KPDQHFKPKYNKHOIPLKRLYANRRIEDHLLVVERRWVARKPLDVKYKPGKCFQGDH 474

QY 484 GYNNPFSMEATFLAHPGSPKEKTEVEDPENTEVNMCDLIRIQLDAPANGTHGSNLHIL 543
D 475 GFDNKVNSMOTVFEYGPYFKYRKVPPFENTILYNTMCNCDLGLKEPKANNTHGSNLHIL 534

QY 544 KVPFVEPSSAREVSKFESVCGFANPLPTSLDCP-PHIQNSTQLEQVQNMNLTOBBITA 602
D 535 RTNTTRPFLPEEVERPNYGMYQSDFLGCTCDDKWPKNKLEBLNKRHTK---GS 590

QY 603 TVKVNLPGPVRVQKNDVHCLLYHREVSFGKAMRMPPMSSTYVQQLGDTSPLPPTV 662
D 591 TEERHLLYGRPAVLRTSYDILYHTDESGYESEIFMLPLWTSYTISKQALVSSIEBHLT 649

QY 663 DCLRADVRPSESGKCSFYSLADKNITHGFLYPPASNTSDSQDALITSNIVPMYBEFR 722
D 650 NCVRDPRVSPGFSQNCLAYKNDQMSGFLFPYSSPEAKYDAFLVNMVPMYPAFK 709

QY 723 KMWDYFHSSVLLKATERGVNTVSGPFDYNDGHEFADPTEKHLLANTDVPJPTHYFV 782
D 710 RWTWTFQRVLYKXASERGVNVNISGPFDYNDGFLRDIEDIKQIVEGSSIPVPHYS 769

QY 783 VLTSCKNSHTBPENCPGMLDVLPTTIPHRPTNVESCPKGKPAWYEEERTAHIAVRYDV 842
D 770 LITSLCLDFTOPADKGDPJVSSTSFILPDRPDNECSNSSEDESKWELMKTHTAVRDR 829

QY 843 ELLTGSDFYDKVQFVSEIQLQKTYLPFETTI 875
D 830 EHLTGSDFYRKTSRSYSEIQLQKTYLPFETTI 862

RESULT 7
ID NPP2_HUMAN STANDARD:
ID NPP2_HUMAN STANDARD:
AC Q13822; Q13822; Q15117;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE (Phosphodiesterase I/nucleotide Pyrophosphatase 2) (Phosphodiesterase I alpha) (PD-Ialpha) (Autotaxin) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide Pyrophosphatase (EC 3.6.1.9) (NPPase)].
DE I (EC 3.1.4.1); Nucleotide Pyrophosphatase (EC 3.6.1.9) (NPPase)].
GN ENPP2 OR PDNP2 OR ATX.
CS Homo sapiens (Human).
CC Ectonucleotide Pyrophosphatase 2 (E-NPP 2)
CC (Phosphodiesterase I/nucleotide Pyrophosphatase 2) (Phosphodiesterase I alpha) (Autotaxin) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide Pyrophosphatase (EC 3.6.1.9) (NPPase)].
CC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;

OX NCBITAXID=9606;
RN [1] SEQUENCE FROM N.A. (ISOFORM 2), PARTIAL SEQUENCE, AND
RP CHARACTERIZATION.
RC TISSUE-Melanoma,
RX MEDLINE=95074054; PubMed=7929564;
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arrestad A.A.,
RA Sobel M.B., Liotta L.A., Stracke M.L.,
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";
RL J. Biol. Chem. 269:30479-30484 (1994).
RN [2] SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Testis;
RC MEDLINE=96158950; PubMed=8579579;
RA Lee H.Y., Murata J., Clair T., Polymeropoulos M.H., Torres R.,
RA Matrull R.E., Liotta L.A., Stracke M.L.;
RT "Cloning, chromosomal localization, and tissue expression of autotaxin from human teratocarcinoma cells.";
RL Biochem. Biophys. Res. Commun. 218:714-719 (1996).
RN [3] SEQUENCE FROM N.A. (ISOFORM 1).
RP MEDLINE=96138999; PubMed=8586446;
RX Kawago H., Sano O., Goji J., Nishitamura N., Narita M., Inazawa J.,
RA Nakamura H., Sano K.,
RT "Molecular cloning and chromosomal assignment of the human brain-type phosphodiesterase I/nucleotide.";
RL Genomics 3:380-384 (1995).
RN [4] SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Testis;
RC MEDLINE=9238257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sheehan C.M., Bhat N.K.,
RA Altchuk S.F., Zeeberg B., Buelow K.H., Schafer C.F.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquejano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Halton E., Ketteman M.C., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.A.C., Grimwood J., Schmutz J., Dickson M.C.,
RA Rodriguez A.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherzer A., Schein J.E., Jones J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
CC -!- FUNCTION: Has a potent tumor cell motility-stimulating activity.
CC -!- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing: Named isoforms=2;
CC Name=1;
CC IsoId=013822-1; Sequence-Displayed;
CC Name=2;
CC IsoId=013822-2; Sequence-VSP 006750;
CC -!- TISSUE SPECIFICITY: Predominantly expressed in brain, placenta, ovary, and small intestine.
CC -!- SIMILARITY: Contains 2 somatomedin-B type domains.
CC ---
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Db	189 IELRSGGTHSPYMPVPPTCFEPNLYTATGLYPBESHGIVGNSMYDPVFEDATHLRLRGE 248
CC	DR EMBL: L35594; AAA64785.1; -.	Qy	244 QNPAAWHQGPMLTANYQDRAATYFWPSEVAINGFFPSIYMPNGVSPFBFRISTL 303
CC	DR EMBL: B008260.1; -.	Db	249 KENHRWGGQPIWITAKQGYKAGFFFW-----SVVIPH-----ERRILTL 290
CC	DR EMBL: BC034961; AAH34961.1; -.	Qy	304 KWLDLPAERPRFITYFEFPDSSSHAGGPSARVTKALQQVDFHAFTGMLKQRNLHN 363
CC	Genev; HGNC:3357; ENPP2.	Db	291 QMLTLPHERPSVATYSEQFDGKSYGFPGPEMTNPRLREIDKVGQLMDGLKQLKLHR 350
MIM: 601060; -.	DR GO; GO:0004551; C: integral to plasma membrane; TAS.	Qy	364 CNTFLILADEGNDOTCNKMEYMTYFRPRNFYMEGSPAPRTR--RAHNPIDFESSNS 420
DR GO; GO:0004528; F-nucleotide diphosphatase activity; TAS.	DR GO; GO:0008134; F-transcription factor binding; TAS.	Qy	475 NTNC-GGGNHGYNNEPRSMEAFLAHGSPSKKEKEVEPFENIETYNLMCDLRLICPDRN 533
DR GO; GO:000928; P-cell motility; TAS.	DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . . ; TAS.	Db	351 CNVIFGDHMEVDTCRTEFLSNLTNTDDITLVPGTGLGRSKFSNNAKYD----P 405
DR GO; GO:0006796; Phosphate metabolism; TAS.	DR InterPro; IPR01604; Endonuclease.	Qy	421 EIVRNLSCKREDQHEPKYLTPLDKRHLHYAKTRIDKYLFLYDQOW----LAVERSKS 474
DR InterPro; IPR002591; Phosphodiest.	DR InterPro; IPR001212; Somatomedin B.	Db	416 KAIJANIDCCKCPDQHEPKYLRQHLPKRLHANNRIEDHLIYERRWHPARKPDVYKP 465
Pfam; PF00223; Endonuclease; B.	DR P000134; F-transcription factor binding; TAS.	Qy	476 SCRCFFGDHGDNKVNNSMQTIVFQYQPTKVKYKRPVPPENIELYNNCDLGLKPNAN 525
Pfam; PF01563; Phosphodiest; 1.	DR P00133; Somatomedin B; 2.	Db	534 GTHGSIHLILKYYEPEPSSAEEVSKEFSGVCGANLPTESLDLFCF- PHIQNQSTOLEQNQM 592
Pfam; PF00022; SOMATOMEDINB.	DR SMART; SM00477; NUC; 1.	Qy	526 GTHGSILHLLTNTTPMPEVTNPYRPMYIQLQSDFLQGCTDDKYPKQNLDELNKR 585
SMART; SM00201; SO; 2.	DR Glycoprotein; PS00324; SOMATOMEDIN B; 2.	Db	593 INLTQEERITAVKVLPGPRPLQOKNDHCLLYREPTYSFGKAMRMPPMASSTYVQQLG 652
KW Glycoprotein; Transmembrane Repeat; Signal-anchor; Hydrolase;	DR Glycoprotein; Transmembrane enzyme; Alternative splicing.	Qy	586 LHTK---GSEERHLLGHAYPAVLYTPEHDLIYHTDPSFGSESEIUNPLWTSYVXQA 640
KW Multifunctional enzyme; Alternative splicing.	FT DOMAIN 1 11 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)	Db	653 DTSPLPTVPCDCLRADVRVPSSSEOKCSFVLAQDNTHFLPPASNETSDQYDALITS 712
FT DOMAIN 12 30 (POTENTIAL)	FT DOMAIN 31 863 EXTRACELLULAR ATTACHMENT SITE (POTENTIAL).	Qy	641 EVSSVPHPLTSCVRPVYRVPSPFSQNCNLAYKNDQMSGFLFPYLSPEAKYDAFLVT 700
FT DOMAIN 13 30 (POTENTIAL)	FT DOMAIN 55 98 SONATOMEDIN-B LIKE 1.	Db	713 NLVPMTYEFKRWDYDPSVLLKHATERGVNVSGPFDYDNYDGHFPADDEITKHLANT 772
FT DOMAIN 14 30 (POTENTIAL)	FT DOMAIN 99 143 SONATOMEDIN-B LIKE 2.	Qy	701 NMVPMYFAEKRVWTFQRLVKKYASERGVNVSGPFDYDIDGLHLTDETKQKYVEGS 760
FT DOMAIN 15 30 (POTENTIAL)	FT DOMAIN 145 502 PROSPHODIESTERASE.	Db	773 DVPIIPTHYFVYLTSCKNSKSHTPENCPGWLPLTTIPHRPTNYESCPGKPEALWVERF 832
FT DOMAIN 16 30 (POTENTIAL)	FT DOMAIN 198 863 NUCLEASE.	Qy	761 SIVPVPHYIYSLTISCLQT PADKCDGPUSVSSETLHPDNESCSNSEDSKWVEELM 820
FT VARSPLIC 1 210 BY SIMILARITY.	FT ACT SITE 120 CELL ATTACHMENT SITE (POTENTIAL).	Db	833 TAHIAARVDRVLLTGIDFYODKVQPVSEIOLKTLYPFTETTI 875
FT VARSPLIC 2 23 N-LINKED (GLCNAC. .) (POTENTIAL).	FT VARSPLIC 23 23 N-LINKED (GLCNAC. .) (POTENTIAL).	Qy	821 KQHTARYRDISHLTSDFRKTSRSYPBLTKTLYHRYSEI 863
FT CONFLICT 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).	FT CONFLICT 73 23 D -> H (IN REF. 1).	Db	RESULT 8
FT CONFLICT 100 100 G -> A (IN REF. 2).	FT CONFLICT 100 23 D -> H (IN REF. 3).	Db	NPP2_RAT STANDARD; PRT; 885 AA.
FT CONFLICT 291 291 Q -> R (IN REF. 1).	FT CONFLICT 291 23 G -> A (IN REF. 2).	ID NPP2_RAT	AC 064610;
FT CONFLICT 349 349 H -> R (IN REF. 1).	FT CONFLICT 349 23 G -> A (IN REF. 2).	DT 28-FEB-2003	(Rel. 41, Created)
FT CONFLICT 629 629 P -> L (IN REF. 1).	FT CONFLICT 629 23 G -> A (IN REF. 2).	DT 28-FEB-2003	(Rel. 41, Last annotation update)
FT CONFLICT 644 644 S -> R (IN REF. 3).	FT CONFLICT 644 23 G -> A (IN REF. 2).	DE (EC 3.1.4.1); Nucleotide Pyrophosphatase 2 (Phosphodiesterase 2)	DE (EC 3.1.4.1); Nucleotide Pyrophosphatase 2 (Phosphodiesterase 2)
FT CONFLICT 703 703 V -> A (IN REF. 3).	FT CONFLICT 703 23 G -> A (IN REF. 2).	DE (EC 3.1.4.1); Nucleotide Pyrophosphatase 1 (nucleotide Pyrophosphatase 1)	DE (EC 3.1.4.1); Nucleotide Pyrophosphatase 1 (nucleotide Pyrophosphatase 1)
FT CONFLICT 769 769 Y -> H (IN REF. 3).	FT CONFLICT 769 23 G -> A (IN REF. 2).	DE (EC 3.1.4.1); Nucleotide Pyrophosphatase 1 (nucleotide Pyrophosphatase 1)	DE (EC 3.1.4.1); Nucleotide Pyrophosphatase 1 (nucleotide Pyrophosphatase 1)
SEQUENCE 863 AA: 99003 MW: 05B8A2E555C464BC CRC64: 63	Query Match Score 2091.5%; Pred. No. 5.3e-142; Mismatches 267; Indels 59; Gaps 10;	OS Rattus norvegicus (Rat).	OS Rattus norvegicus (Rat).
9 SCGCRKIKCFDASEF 63	Best Local Similarity 43.1%; Matches 388; Conservative 176; Mismatches 267; Indels 59; Gaps 10;	OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthidae; Rodentia; NCBITaxonID-10116;	OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthidae; Rodentia; NCBITaxonID-10116;
64 RGLENCRCVACKDRGDCWDFDTCYESTIWMCNKFRCGEBTRIASLSCSDICLQR 123	Query 14 RGLENCRCAVACKDRGDCWDFDTCYESTIWMCNKFRCGEBTRIASLSCSDICLQR 123	RN SEQUENCE FROM N_A.	RN STRAIN-Sprague-Dawley; TISSUB=Brain;
69 AGPDPCCRCLNLCYSYTSCCHDFDELLKTAARGWECTYKDRCEVRENAEHCSEDCCLARG 128	Query 124 DCCADYKSYCQGETSWLBNCDTAQQSCPEGFDLPPVILSMGDGRAEYLYTWTDLMN 183	RC MEDLINE=9510605; PubMed=7961762;	RC RA Narita M., Goji J., Nakamura H., Sano K.;
Db 9 DCCATNYQVCKGSHWWDDCEIKAECPAGEVRPLIFTSVDFGRASMYKKSCKWNPN 188	Query 129 DCCATNYQVCKGSHWWDDCEIKAECPAGEVRPLIFTSVDFGRASMYKKSCKWNPN 188	RT "Molecular cloning, expression, and localization of a brain-specific phosphodiesterase I/nucleotide pyrophosphatase (PD-1alpha) from rat brain";	RT RL J. Biol. Chem. 269:28235-28242 (1994).
Qy 184 INLKLTGIGHSKYMARMYPTKFPNHYTIVTGLYPSBHGIDDNMMYDVNLNKNSLSSKE 243	Qy 184 INLKLTGIGHSKYMARMYPTKFPNHYTIVTGLYPSBHGIDDNMMYDVNLNKNSLSSKE 243	Qy 184 INLKLTGIGHSKYMARMYPTKFPNHYTIVTGLYPSBHGIDDNMMYDVNLNKNSLSSKE 243	Qy 184 INLKLTGIGHSKYMARMYPTKFPNHYTIVTGLYPSBHGIDDNMMYDVNLNKNSLSSKE 243

CC -!!- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides
CC successively from the 3' hydroxy termini of 3'-hydroxy-terminated
CC oligo-nucleotides.
CC -!!- CATALYTIC ACTIVITY: A dinucleotide + H(2)O = 2 mononucleotide.
CC -!!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!!- TISSUE SPECIFICITY: Abundantly expressed in cerebrum and
cerebellum. Localized in secretory epithelial cells in the brain
and the eye including choroid plexus epithelial cells, ciliary
epithelial cells, iris pigment epithelial cells, and retinal
pigment cells.
CC -!!- SIMILARITY: Contains 2 somatomedin-B type domains.

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or send an email to licensee@isb-sib.ch).

CC EMBL: D28560; BRA05910.1; - .
CC PIR; A55453; A55453 .
DR InterPro; IPR01604; Endonuclease.
DR InterPro; IPR00591; Phosphodiester.
DR InterPro; IPR001212; Somatomedin_B.
DR Pfam; PF01223; Endonucleases; 1.
DR Pfam; PF01653; Phosphodiester; 1.
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00921; SOMATOMEDIN_NB.
DR SMART; SM00477; NUC; 1.
DR SMART; SM00201; SO; 2.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
KW Glycoprotein; Transmembrane; Repeat;
KW Multifunctional enzyme.
FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 12 30 SIGNAL ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT SITE 126 128 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 885 SOMATOMEDIN-B LIKE 1.
FT DOMAIN 54 97 SOMATOMEDIN-B LIKE 2.
FT DOMAIN 98 142 PHOSPHODIESTERASE.
FT DOMAIN 144 499 NUCLEASE.
FT DOMAIN 620 895 BY SIMILARITY.
FT ACT SITE 207 207 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 126 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 829 829 N-LINKED (GLCNAC. .) (POTENTIAL).
ST SEQ 885 AA; 101309 MW; 8C5CA0RC5200793 CRC64;

Query Match Score 2043.5; DB 1; Length 885;
Best Local Similarity 41.7%; Pred. No 1.5e-138; Indels 79; Gaps 12;
Matches 380; Conservative 1/8; Mismatches 275;

3 RQGCGUSFQTLFFAI ---SYNCLQPTASTIKVALLIVMSLGLGLGLRKLEK-----QSC 54
55 RKKCPDASFRGLENCRQDACKDRGDCMDFEDTCVESTRIMCNKFCGETPLEASICS 114
59 KGRCEFLQEQGPDCRDNLCKSSCDBFDELCLKTYRGWECTKDSGEVNEENACH 118
SEQUENCE

14 KKNTLKKYKTAIVLAVLIVMSLGLGLGLRKLEK-----QSC 54
115 CSDDCLQKRUOCADYKSVCOGETSLLENDTAQOSQCDCEGDL - PIVLISMDGFAE 172
119 CPEDCLSRGDCCTNYQVVCGEHRY---DDAARNQSESCLOVCPPLUJISVDGFAS 174
173 YLYTWDLMPNJKURTGTHSKYRMAYPTKTFPNHHTIVTGLYPSHGIDNNMYDN 232
175 YMKGKSRKVMPIEKDRSGTHVPIITRPVTPFKTPNLYIATGHYPESHGIVNSMHPV 234

QY	233 LNKNFSLSSKEQNPNPAWHGQEMWLAMYQGLKAATYFWPGSEVAINGSFPSSYMEYNGS 292
Db	235 FDASFHURGREFHNHRGGQLWIAITQGVRAFGML 352
QY	239 VPEERISTLKLKDILKAKERREPYTMFEFDSSCHAGGPVSARYVKALQYVDAHAFML 352
Db	277 IPBERRITLILQWLSLPNERPSVAYFSEQDFSHKYGPGPENTINPLREIDTKVGQL 336
QY	353 MEGIQRNLHANCYNTILLADHGMQTCQNREBYMTDFPRINFFYMEGAPRIRAHNIP 412
Db	337 MDLKLQPLHRCYNTVFLAHPSPKEKTEVEPPENIEVYNMCDLL 514
QY	526 RIQPAPNNGTHGS1NH1LKVPPYBPSHAEEVSKFSCFGFANPLPTESLDFCF - PHLNQNST 584
Db	515 GLKPKAPPNNTGHS1NH1LRTNTRPIMDEVSRNPNYPMIYLOSEPDLGCTDDKVERKN 574
QY	585 QLEQVNQMLNL ---TQEELTATVYV - ---TQEELTATVYV - ---NLPFGPRVRVLQKNYDHC 623
Db	575 KLEBLNKRULHTKGSTEATGKFRCGSKENKNTONGSYEPRKEERHLYGRPAVLR - TSYD 633
QY	624 LYIHYREYVSGFGRAMRMPWSSYTVPQUDTSPLPPTVDPCLRADVWYRPPSESOKCSYL 683
Db	634 ILYHTDPESSGYSELFMLPLWTSYTISKQAEVSSSPEHLTNQVRDPDVRSQGFQNCLAYK 693
QY	684 ADKNITHGFLYPPASNRTSDQYDALITSNLVPMYEPRKMWDYFHSVLLIKEATERNGV 743
Db	694 NDKQNSYGFLEPPPLSSSPEAKYDAFLVNMMVPAKRVWASYFQRLVKKYASERNGV 753
QY	744 NVVSGSPIFDYNYDGFDADEITGHANTDVP1PTHYPVVLTSCKNSHTPENGPWLDDV 803
Db	754 NVVSGSPIFDYNYDGRDTEDEIKOVVEGSSIPVTHYNSIITSLDFTQPADKCDGPLSV 813
QY	804 LPFIPLHRPTNVESCGPKPEALWYEERTAHTARVDRVELLTGIDFYODKVQPSSEILQ 863
Db	814 SSF1PLHRPNDDESSDEKVNTEELNMKHTARVDR1EHLTSLDFYRKTTSYSSEILT 873
YCR6 YEAST	ID YCR6 YEAST STANDARD; PRT; 742 AA.
AC	P23355; QBNI99; P25355; QBNI99;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-OCT-2003 (Rel. 42, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Hypothetical protein YCR026C.
GN	YCR026C OR YCR46.
OS	Eukaryotes cerevisiae (Baker's yeast).
NCBI TaxID	4932;
RN	SEQUENCE FROM N.A.
RC	STRAIN=S288c;
RC	MEDLINE=922443566; PubMed=1574125;
RA	Oliver S.G., van der Aart O.J.M., Agostoni-Carbone M.L., Aigle M.,
RA	Alberghina L., Aleksandraki D., Antoine G., Pawar R., Ballesta J.P.G.,
RA	Bent P., Berben G., Bergantino E., Bites N., Boile P.-A.,
RA	Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,
RA	Carignani G., Chanet R., Contreras R., Crouzet M., Daugman-Fornier B.,
RA	De Haan M., Defoor E., Delgadillo M.D., Demolder J., Doira C., Dubois E.,
RA	Dujon B., Duesterhoeft A., Erdmann D., Estebaran M., Fabre F.,

Matches	126; Conservative	72; Mismatches	154; Indels	95; Gaps	22;	QY	167	DGFPEAYLYTWDLMPNINKLTKCGISKYNRAMPYPTKTFENHYTIVTGLYPESHGIDN 226
QY	150 SQCPGEGRDLP-----VILFSMDFRAEYL---YTWTDLMPNINK 186					Db	1	DGFPEAYLYTWDLMPNINKLTKCGISKYNRAMPYPTKTFENHYTIVTGLYPESHGIDN 60
Db	47 SKCPKPIDNGERTIANTSNTYFNGTHDFKTLTLLISDFHPLIDAKYT--PFLNLHN 104							
QY	187 LKTCG---TESKYKRAMYTKTKEPNHYTIVTGHYPEBRGITIONNMVNUNLNKNFNSLSK 242					RESULT 12		
Db	105 LRSPPDMNNTATPNNIPSPTQTFPNHNSWNTGKPIBHGIVSNIFWD----NFISSEF 159					TNAG_HUMAN	STANDARD;	PRT;
QY	243 EQNN---PAWHD-GQPWW-LTAMYQG-LKAATFPPGSEVAI--NGSFPsiMP---- 288					ID	Q9UW2W ; Q9UW1W ; Q9ULZ4 ;	
Db	160 RPNNDARINNTAIPWQLQQTSSQGETYKVATHMWPGSSEVHHGG-- PVSARVIALQVV 219					DT	10-OCT-2003 (Rel. 42, Last sequence update)	
QY	289 YNGSVPPFEERISTLKWLDLPK-AERPFRTYMFEEPDSSGHAGG-- 345					DT	10-OCT-2003 (Rel. 42, Last annotation update)	
Db	220 FNQWEKLQDQLAQIRYIDMNLQQLDPLRRELVISYI.PNVSYGHSGFGYDLDRKLQKLGEV 279					DB	DB	
QY	346 DHAFCMILEGKQRLNHCNLLILLADKMDQDTCQNNEAYMTY-- FPR----TINFF 396					GN	TNAC.	
Db	280 DGFFLDLIEGLQKRNLLKINVNMTSDHGMNSNTANDSEHVVWERYTPADAMSAFISHL 339					RN	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.	
QY	397 YMVEGDPAPRRAHNIPHDFFSFNSNEEVNLSCRKPKDHFKPYLTDPDKRHL----- 449					RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.	
Db	340 Y-NEGMMYMMCLKN-PRD-----KQWICDLIEAQLRKYAGDELSRKRFHVILKEDF 387					RC	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.	
QY	450 -----YAKNVRIDKVLHLEVDQOWLAVERSKSNTNCG-GNGYN-NEFRMEA 494					RX	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.	
Db	388 DPSWKYFYQDNRKHRDYDRGDIWILADEYYATIVKEMGDVPIGMGTGYNENNCSDDAS 447					RX	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.	
QY	495 IFLAHGSPFKEKTEVEPFENIEVYNNL 521					RX	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.	
Db	448 IFIGMGPMPNTEV-VPPPENIEVYNNL 473					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
RESULT 11						RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
PPDI_BOVIN	PPDI_BOVIN STANDARD;	PRT;	61 AA.			RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
AC	P15356;					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
DT	01-APR-1990 (Rel. 14, Created)					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
DT	01-APR-1990 (Rel. 14, Last sequence update)					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
DT	28-FEB-2003 (Rel. 41, Last annotation update)					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
DE	Phosphodiesterase I (EC 3.1.4.1) (5'-exonuclease) (5'-nucleotide phosphodiesterase) (Fragment).					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
DS	Bos taurus (Bovine).					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
OC	Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bovinae; Bos.					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
OC	NCBI_TaxID:9913;					RX	"Identification of two alternatively spliced forms of human tubulointerstitial nephritis antigen (TIN-Ag)." [2]	
BN	[1]. IN SEQUENCE.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
RP	KIDNEY INT.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
RC	TISSUE=Intestine;					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
DIS	DISASE.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
RA	MEDLINE=83234541; PubMed=22989287;					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
RA	Culp J.S., Blytt H.J., Hermodson M., Butler L.G.; Butler A.F.; Charonis A.S.; Chen Y., Krishnamurti U., Wayner B.A.; Santamaría P., Nevins T.E., Kim Y., Butkowski R.J.; Kleppel M.M.; Katz A.; Michael A.F.; Fish A.J.; Am. J. Med. 93 :691-698(1992).					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
RT	"Amino acid sequence of the active site peptide of bovine intestinal 5'-nucleotide phosphodiesterase and identification of the active site residue as threonine." [4]					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
RT	J. Biol. Chem. 260:18320-18324(1985).					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
CC	-!- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
CC	PIR; A25274; A25274.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
DR	DR Pfam: PF01663; Phosphodiester; 1.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
KW	Hydrolease.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
FT	NON_TER 1 ACT SITE 39 PHOSPHOTHREONINE INTERMEDIATE.					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
FT	SEQUENCE 61 AA; 6999 MW; 580CB4807A61C84 CRC64;					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
SQ	Score 301; DB 1; Length 61;					RX	"Distribution of tubulointerstitial nephritis antigen and evidence for multiple forms." [3]	
Query Match	6.3%; Best Local Similarity 86.7%; Matches 52; Conservative 4;	Pred No. 2.8e-15; Mismatches 4; Indels 0; Gaps 0;				RX	DEVELOPMENTAL STAGE.	
						RX	MEDLINE=98303799; PubMed=9643646;	
						RX	"Receptors in proximal tubular epithelial cells for tubulointerstitial nephritis antigen";	
						RX	Kidney Int. 49:155-157(1996). [7]	
						RX	"Tubulointerstitial nephritis antigen (TIN-ag) is expressed in	

RRT
 Connect. Tissue Res. 37:53-60(1998).
 -!- FUNCTION: Mediates adhesion of proximal tubule epithelial cells
 via integrins alpha3-beta1 and alphaV-beta3.
 -!- SUBCELLULAR LOCATION: Basement membranes.
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=TININ;
 IsoID=99UYU7W-1; Sequence=Displayed;
 Note=Major isoform;
 Name=TININ;
 IsoID=99UYU7W-2; Sequence=YSP_050567, YSP_050568;
 -!- TISSUE SPECIFICITY: Expressed in the kidney cortex, small intestine and cornea.
 -!- DEVELOPMENTAL STAGE: Initially observed in the Bowman's capsule during early glomerular capillary loop formation in the kidney. In more developmentally mature glomeruli, following transition from early to mid-capillary loop stage, expression is higher in the proximal tubular basement membrane than in the distal basement membrane and Bowman's capsule.
 -!- DISEASE: Antibodies against TINAG are found in sera of patients with tubulointerstitial nephritis, a rare autoimmune disorder that causes acute and chronic renal injury.
 -!- SIMILARITY: Belongs to Peptidase family C1.

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TE		Alternative splicing.		Cleavage (by furin)		(POTENTIAL).	
ARBOHYD	38.	49	50	N-LINKED (GLCNAC.	.)	(POTENTIAL).	
ARBOHYD	175.		38	N-LINKED (GLCNAC.	.)	(POTENTIAL).	
ARBOHYD	314		175.	N-LINKED (GLCNAC.	.)	(POTENTIAL).	
ARBOHYD			314	N-LINKED (GLCNAC.	.)	(POTENTIAL).	

CARBON	360	360	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	455	455	N-LINKED (GLCNAC. . .) (POTENTIAL).
VARSPLIC	119	169	Missing (in Isoform TIN2).
			/FTid=VSP 050567.
VARSPLIC	209	300	Missing (in Isoform TIN2).
			/FTid=VSP 050568.
CONFLICT	7	8	FS -> IL (IN REF. 1).
CONFLICT	175	175	N -> I (IN REF. 2; AAFF08932).
CONFLICT	199	199	P -> L (IN REF. 1).
CONFLICT	333	333	D -> H (IN REF. 1).
CONFLICT	381	381	R -> H (IN REF. 1).
CONFLICT	421	421	L -> R (IN REF. 2; AAFF08932).
CONFLICT	437	437	P -> S (IN REF. 1).
CONFLICT	463	463	V -> I (IN REF. 1).
SEQUENCE	4/16 AA:	54/64 MW:	>22DE8B3308C3077 CRC64.

Query	Match	2.7%	Score	130;	DB	1;	Length	476;
	Best Local Similarity	21.4%	Prod. No.	0.083;				
	Macches	56;	Conservative	29;	Mismatches	69;	Indels	108;
							Gaps	13;
Qy	75	CKDRDCCMWFDFPCTESTRIMCNKPRGEGTRLEASILCSDDC-LQKDCCADYKSV	C	V	133			
Db	57	CRNFG-CCEDRDDGCV-TEFYAN-	A	L	133	Y	C	CPDKSF
Qy	134	QGETSW-----	E	E	162	N	N	102
Db	103	REEKEWPHTQPMPYPEGFPDKGHYEGSVIRENCNSCTCSQQWNSCSQHVCLVRPELIE	R	R	162	Y	Y	
Qy	163	-----LFSMDGPRAEYLWDDLMNPINKLKTGITSKYMAMYPT	S	S	203	Y	Y	
Db	163	QVAKGDXWTAQNYSQFWGMMLTDELGFK-----FRLGTLPSSPMLLS-----MNEMATSLPA	T	T	213	Y	Y	
Qy	204	KTFPNHYTIVTGYPSE-SHG1ID-----	H	H	238	N	N	
Db	214	TTDIPPEFFVASYKWPWTHGPGLDQRKCAASWAFTASAADRIATSKGRYTAHLSPQNL	I	I	238	Y	Y	
Qy	239	LSSEKQN-----NPAPWH	N	N	251	Y	Y	
Db	274	ISSCKAURHGCNGSGLDRAWWY	S	S	295	Y	Y	

RESULT 13					
PP11_HUMAN			SEQUENCE FROM N.A., AND SEQUENCE OF 19-29.		
ID	STANDARD;	PRT;	SEQUENCE FROM N.A., AND SEQUENCE OF 19-29.		
PP11_HUMAN			SEQUENCE FROM N.A., AND SEQUENCE OF 19-29.		
AC	PP11_28;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 1, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Placental protein 11 precursor (EC 3.4.21.-) (PP11).				
OS	Homo sapiens (Human).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TAXID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 19-29.				
RC	SEQUENCE_Placenta;				
RX	MedlineB=90174895; PubMed=2350438;				
RA	Grundmann U., Roemisch J., Siebold B., Bonn H., Amann E.;				
RT	"Cloning and expression of a cDNA encoding human placental protein 11, a putative serine protease with diagnostic significance as a tumor marker."				
RT	DNA Cell Bank 0-213 25/10000				
PI					

[2] SOMATMEDIN-B TYPE DOMAIN, MEDLINE=91248172; PubMed=1710108; Jenne D.; "Homology of placental protein 11 and pea seed albumin 2 with vitronectin;" *Biochem. Biophys. Res. Commun.* 176:1000-1006(1991).

-|- FUNCTION: Probable serine protease.

-|- MISCELLANEOUS: PLACENTAL PROTEIN 11 IS A PLACENTAL-SPECIFIC PROTEIN BUT IS ALSO ASSOCIATED WITH VARIOUS MALIGNANT NEOPLASMS.

-|- SIMILARITY: Contains 1 somatomedin-B type domain.

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EMBL: M32402; AAA64641;
EMBL: M36109; AAA64651;
PIR: A34614; A34614.
MIM: 606720;
GO: GO:0005615; C:extracellular spaces; TAS.

DR	InterPro; IPR001212; Somatomedin_B.	RN	Nature 413:523-527(2001).
DR	Pfam; PF0103; Somatomedin_B; 1.	RP	[2] SEQUENCE FROM N.A.
DR	SMART; PR00022; SOMATOMEDIN_B.	RC	STRAINKIMS / Biovar Mediævalis;
DR	SM00201; SO; 1.	RX	MEDLINE=22137863; PubMed=1142430;
DR	PROSITE; PS00524; SOMATOMEDIN_B; 1.	RA	Deng W., Burland V., Plumbett G., III, Boutin A., Mayhew G.F., Liss P.,
DR	KW Hydrolase; Serine protease; Signal; Polymorphism.	RA	Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
FT	SIGNAL 1 18 PLACENTAL PROTEIN 11.	RA	Fetherston J.D., Lindner L.E., Brubaker R.R., Plano G.V.,
PT	CHAIN 19 369 SOMATOMEDIN_B-LIKE.	RA	Serraley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
PT	DOMAIN 45 89 E->Q (in dbSNP:6504).	RA	Perry R.D.
PT	VARIANT 31 31 /FTid=VAR_014733 /dbSNP:6505).	RT	"Genome sequence of <i>Yersinia pestis</i> KIM.";
PT	VARIANT 31 31 E->V (in dbSNP:6505).	RL	J. Bacteriol. 184:4601-4611(2002).
FT	/FTid=VAR_14734 /dbSNP:6505).	CC	- - SIMILARITY: Belongs to the UPF0192 family.
SQ	SEQUENCE 369 AA: 42121 MW: F5935AE12D7E924C CRC64;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Qy	53 SCRKKCFDASFRGLENCRDIYACKDRODCCMVDFFEDTCVESTRIMCNKFRGETPLEASL 112	CC	EMBL: A7414152; CAC91375; 1 :-
Db	48 SCGRCRYEA-FDKHHQHCHCNARCQEFGNCCRDPELSICSDHE-----87	CC	EMBL: AE013717; AAM84721; 1 :-
Qy	113 CSCDDDC1QKDCCADYKSVCOGETSMLE-----ENC---DTAQQ-SQCPEGFDLP 159	DR	DR PIR: AC0314; AC0314.
Db	88 VSHSSDAITKEE-QSISRKIYADTKNAQKDIVLNQNCTISPETRNQYDRCRCPK-----143	KW	Signal: Complete proteome.
Qy	160 PTILESMDFRAEYLWMTDLMPNINKTCGIHSKYMARMYPTKTFPHHYTTIVTGLYPE 219	PT	POTENTIAL.
Db	144 ---LFT--YNNELKFLKRPYTAFINL-----ANNQRATG----173	FT	HYPOTHETICAL PROTEIN YP02573.
Qy	220 SHGLIDNNMYDVNLNKNSPLSSKKEONNPFAWWGQPMWLTAMYQGLKAATYFWPGSEVAIN 279	SQ	SEQUENCE 2004 AA; 224130 MW; EA9F8A1E7452672C CRC64;
Db	174 -HG-----EHSAQELAEOQAFL--REFMTAVMKELY-----203	CC	Query Match 2.6%; Score 126; DB 1; Length 2004;
Qy	280 GSFBPSIYHNGSYVPFERIYSTLLKWLDPKAERPRPYTMFEEDPSGHAGGPYSARI 339	CC	Best Local Similarity 19.7%; Pred. No. 1.1;
Db	204 -SFLHHQHRYGSQEFVDDLNKM--WFCL-----YSRGNEEGLOSSG-----241	CC	Matches 131; Conservative 89; Mismatches 258; Indexes 31;
Qy	340 KALQVVDHAEGMMEGLKORNHLNCVNILLADHGMDOCTYCNRMETMDYPRINPFMY 399	Db	283 NFSVYDEKRLKWDLDEKAERPRFTYMFEEPDSSGHAGGPVSARVIALQVVDHAFG----350
Db	242 -----FEHVPSGEVKKGTVGFHNWRE-----YLEEKEGLVYYISHI-----Y 280	Qy	295 FEERISTLKLWNLDEKAERPRFTYMFEEPDSSGHAGGPVSARVIALQVVDHAFG----350
Qy	400 EGP 402	Db	325 ATPTQANQKRVWSV-----PNLYSL-----AVNSINATLVE-----DNNGERAL 365
Db	281 DGP 283	Qy	351 -MILEGLKQRLHICVNILLADHGMDOCTYCNRMETMDYPRINPFY-----391
Qy	RESULT 14	Db	366 HIAISDAVKDKEIKAIVAKMLPQNFQAKESAKTS-----TDFYPMDDDDNNLQQSTPL 423
ID	YP73_YERBE STANDARD; PRT; 2004 AA.	Qy	392 --RIN-----PEFMYEGPAPPIRAHNIPHDFFSNSEEEIVRNLSCKRKPDQHKPKYI 440
AC	Q8ZJ2;	Db	424 ALTRIBAEQYOPISFKFADPSYRTLLIVNNSTTSVGGYKM-----PEKIQIVR 475
DT	28-FEB-2003 (Rel. 41, Created)	Qy	441 TPDLPKRLHYAKNTRIDKWHFVDOQWLAVRSKSNTNCGGNHGYNNFRSMEAFLFLAHG 500
DT	28-FEB-2003 (Rel. 41, Last sequence update)	Db	476 VPDPYKTLRFMSOGSL--LSMQGDQ-ISAARNNT-----GMKLDIKRVPSQLQHI 525
DE	Hypothetical protein YP02573 precursor.	Qy	501 PSFKEKEVERFENIVNMCDLRIPQAPNNNGTHGSINH-----541
GN	YP0573 OR Y143.	Db	526 VSFKSEYYSSAHFNRLSDEYFTEHQYQTALNNDPGEINYQGVDSLRSYANNPSARRGV 585
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Qy	542 -LKKPFYEP-----SHAEE-----VSKPSVCGFANPLTESLLFCPCPQLNST 584
OC	Enterobacteriaceae; Yersiniae.	Db	586 FULLISAWDPEKRDNQHQSESDYDQEWNQDSRVITDGLGITKQSOD----RSRDV 640
OX	NCB_1_TaxID=632;	Qy	585 QLEQVNQMLNLTQEELITAVKVNLPFGGRPRVLYKNVDHCLLYHREYVSGFGKAMRPMWS 644
RP	SEQUENCE FROM N.A.	Db	641 FVQSTHSGLPAADAKYVVAKNGNV-----LISQITDSKGVHVFPAIDAF-KNERPVL- 692
RX	STRAINCO-92 / Biovar Orientalis;	Qy	645 SVTPQLGDTSPLPPTVY-----DCLRADV-RVPPSESQCSKFYL-ADKNITHGLYPP 696
RA	MEDLINE=21470113; PubMed=11586360;	Db	693 M1VKEGDSVSEPTTRAYDRNLDIFSRDGEETPSDPRTLSSYIFSDRVS-----744
RA	Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Baker S., Basham D., Bentley S.D., Brooks K., Churcher C., Mungall K.L., Project M.B., Sebaihia M., James K.D., Cerdeno-Tarzaga A.M., Chillingworth T., Cronin A., Davies R.M., Davis J., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moulle S., Oyston P.C.E., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,	Qy	697 ASNTRSDSQYDALITSNL-----VPMYBFRKWDYFHSVLLKHATERNGNVVS- 747
RA	"Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague"; RT	Db	745 -YRPGBRFNIGLITRTANWATLDGYPLRAIRDPRDTLMSTLPI-TLDSGGNELSY 800

QY 748 ----GPIFFDYN-YDGHFFDAPDEITKHILANTDVF----PTHYFVVLTSCKNRSHTPENC 797
 Db 801 TTGENSPPTGWNVLYLGKONNETSMILGGTTVNKEPEPDRLKQVL----QLTPER 854

Qy 798 PGWL 801
 Db 855 QGWR 858

RESULT 15
 LRP1_CHICK STANDARD; PRT; 4543 AA.

AC P98157;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Low-density lipoprotein receptor-related protein 1 precursor (LRP)
 DB (Alpha-2-macroglobulin receptor) (A2mR).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX NCBI_TaxID=9031;
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=White leghorn; TISSUE=Liver, and Ovary;
 MEDLINE=9410321; PubMed=7506255;
 RA Nimpf, S.; Bilous, P.T.; Schneider, W.J.;
 RT "The somatic cell-specific low density lipoprotein receptor-related
 protein of the chicken. Close kinship to mammalian low density
 lipoprotein receptor gene members";
 RL J. Biol. Chem. 269:212-219(1994).
 CC -!- FUNCTION: Involved in the plasma clearance of chylomicron remnants
 CC and activated alpha 2-macroglobulin, as well as the local
 metabolism of complexes between plaminogen activators and their
 CC endogenous inhibitors. Binds vitellagenin, calcium and alpha 2-
 CC macroglobulin.
 CC -!- SUBCELLULAR LOCATION: Type I membrane Protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoID=P98157-1; Sequence=Displayed;
 CC Name=2;
 CC IsoID=P98157-2; Sequence=VSP_004312;
 CC -!- TISSUE SPECIFICITY: Somatic.
 CC -!- PTM: Cleaved into a 85 kDa membrane-spanning subunit (LRP-85) and
 CC a 515 kDa large extracellular domain (LRP-515) that remains non-
 CC covalently associated.
 CC -!- SIMILARITY: Contains 22 EGF-like domains.
 CC -!- SIMILARITY: Contains 31 LDL-receptor class A domains.

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CC EMBL; X74904; CMAS2870/1; -.
 DR PIR; A53102; A53102.
 DR PDB; 1LPX; 29-DEC-99.
 DR InterPro; IPR000152; Asx_hydroxy1_S.
 DR InterPro; IPR01881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR02172; LDL_receptor_A.
 DR InterPro; IPR002172; LDL_receptorRep.
 DR Pfam; PF00008; EGF_F14.
 DR Pfam; PF00057; Ldl_recept_a.
 DR Pfam; PF00058; Ldl_recept_b.
 DR PRINTS; PR0026; LDLRECEPTOR.
 DR SMART; SM00192; EGF_Ca; 3.
 DR SMART; SM00135; LY; 34.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_F1; 5.
 DR PROSITE; PS01186; EGF_F2; 7.
 DR PROSITE; PS50026; EGF_F3; 8.
 DR PROSITE; PS01187; EGF_Ca; 2.
 DR PROSITE; PS01209; LDLRA_1; 27.
 DR PROSITE; PS50068; LDLRA_2; 31.
 KW Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein; Signal;
 KW Calcium-binding; EGF-like domain; Coated pits; Alternative splicing;

KW 3D-structure; 1 21
 FT SIGNAL 1 21
 FT CHAIN 22 4543
 FT DOMAIN 22 4419
 FT TRANSMEM 4420 4443
 FT DOMAIN 4444 4543
 FT DOMAIN 27 68
 FT DOMAIN 72 112
 FT DOMAIN 113 151
 FT DOMAIN 152 191
 FT DOMAIN 476 522
 FT DOMAIN 801 841
 FT DOMAIN 850 890
 FT DOMAIN 891 931
 FT DOMAIN 932 971
 FT DOMAIN 972 1011
 FT DOMAIN 1011 1051
 FT DOMAIN 1058 1097
 FT DOMAIN 1100 1140
 FT DOMAIN 1141 1180
 FT DOMAIN 1181 1220
 FT DOMAIN 1221 1260
 FT DOMAIN 1534 1577
 FT DOMAIN 1842 1883
 FT DOMAIN 1883 2151
 FT DOMAIN 2151 2191
 FT DOMAIN 2472 2512
 FT DOMAIN 2516 2557
 FT DOMAIN 2558 2596
 FT DOMAIN 2597 2635
 FT DOMAIN 2636 2684
 FT DOMAIN 2688 2730
 FT DOMAIN 2730 2769
 FT DOMAIN 2770 2812
 FT DOMAIN 2814 2853
 FT DOMAIN 2854 2897
 FT DOMAIN 2900 2938
 FT DOMAIN 2939 2978
 FT DOMAIN 2979 3019
 FT DOMAIN 3287 3328
 FT DOMAIN 3329 3368
 FT DOMAIN 3369 3407
 FT DOMAIN 3408 3447
 FT DOMAIN 3448 3488
 FT DOMAIN 3489 3530
 FT DOMAIN 3531 3569
 FT DOMAIN 3570 3608
 FT DOMAIN 3608 3646
 FT DOMAIN 3649 3659
 FT DOMAIN 3659 3730
 FT DOMAIN 3736 3776
 FT DOMAIN 3779 3821
 FT DOMAIN 3828 3859
 FT DOMAIN 4146 4182
 FT DOMAIN 4195 4231
 FT DOMAIN 4231 4267
 FT DOMAIN 4267 4303
 FT DOMAIN 4303 4339
 FT DOMAIN 4339 4374
 FT DOMAIN 4372 4409
 FT SITE 3942

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

MM protein - protein search, using sw model

run on: July 6, 2004, 12:45:12 ; Search time 64 Seconds
(without alignments)

3862.954 Million cell updates/sec

title: US-10-005-480A-743

perfect score: 4804

Sequence: 1 MESTLTLATEQPVKNTLKK.....QFVSEIILQLKTYLPPIFETTI 875

scoring table: BLOSUM62

Gapo: 10.0 , Gapext 0.5

15861.07 seqs, 28254/1505 residues searched:

ALIGNMENTS

Cost-processing: Minimum Match C%

```
Maximum Match 100%  
Listing first 45 summaries  
  
database : A_Geneset_29Jan04:  
1: geneset1980s:  
2: geneset1990s:  
3: geneset2000s:  
4: geneset2001s:  
5: geneset2002s:  
6: geneset2003s:  
7: geneset2003bs:  
8: geneset2004s:  
9: geneset2004bs:
```

No. is the number of results predicted by chance to have a score greater than or equal to the score of the total distribution.

סבבון

Result No.	Query			DB	ID	Description	
	Score	Match	Length				
1	4804	100.0	875	7	ADE656099	Human	Pro
2	4804	100.0	875	7	ADE656103	Human	Pro
3	4804	100.0	875	7	ADE65891	Human	161
4	4804	100.0	875	7	ADE65904	Human	161
5	4804	100.0	875	7	ADE65969	Human	161
6	4804	100.0	875	7	ADE65899	Human	161
7	4804	100.0	875	7	ADE65983	Human	161
8	4804	100.0	875	7	ADE65982	Human	161
9	4804	100.0	875	7	ADE65999	Human	161
10	4804	100.0	875	7	ADE65984	Human	161
11	4804	100.0	875	7	ADE65991	Human	161
12	4801	99.9	875	7	ADE65910	Human	161
13	4801	99.9	875	7	ADE65905	Human	161
14	4801	99.9	875	7	ADE65893	Human	161
15	4798	99.9	875	7	ADE65897	Human	161
16	4798	99.9	875	7	ADE65907	Human	161
17	4797	99.9	875	7	ADE65906	Human	161
18	4797	99.9	875	7	ADE65895	Human	161
19	4796	99.8	875	7	ADE65901	Human	161
20	4795	99.8	875	6	AB744664	Human	ect
21	4743	98.7	895	4	AB710289	Novel	hum
22	4642	96.6	841	7	ADE65989	Human	161
23	4642	96.6	841	7	ADE65903	Human	161
24	4634	96.5	841	7	ADE65990	Human	161

RESULT 1

ADE56099 ADE56099 standard; protein; 875 AA.
 ID ADE56099
 XX
 AC ADE56099;
 XX
 DT 29-JAN-2004 (First entry)
 XX
 DE Human Protein AAC51813, SEQ ID NO 11
 XX
 KW Human; pain; neuronal tissue; gene
 KW spinal segmental nerve injury; chromo-
 KW spared nerve injury; SNI; Chung;

27-FEB-2003

XX
PP 14-AUG-2002; 2002WO-US025765
XX
PP 14-AUG-2001; 2001US-US-03121477
PR 01-NOV-2001; 2001US-US-03463822
PR 26-NOV-2001; 2001US-US-03333477
XX
(GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C , D'urso D , Beffort
PA XXX
WPI : 2003-268312/26.
DR GENBANK; AAC51813.
XXX
PR New composition comprising the
PP preparing a medicament for the
XXX
PS Claim 1: Page: 10/11pp; English
XXX
The invention discloses a composition
CC or human polynucleotides or
CC derivative or allelic variants
CC claimed are a vector comprising
CC comprising the vector, a method
CC which is differentially regulated
CC kit to perform the method, a
CC that increases or decreases
CC that is differentially expressed
CC that is differentially expressed
CC

subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.

subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .	Sequence 875 AA;
QY	721 FRKWDYFHSVLLIKHATRERGNYNVSGPFDYDNYDGHDADPEITKHLANTDVPPIPTHY
Db	721 FRKWDYFHSVLLIKHATRERGNYNVSGPFDYDNYDGHDADPEITKHLANTDVPPIPTHY
QY	781 FVVLTSCKNKSHTBPNCPGMWLVLPFLPHRPTVNESCPEGKDEALAYVEERFTAHIAVR
Db	781 FVVLTSCKNKSHTBNCPEWLDVLPFLPHRPTVNESCPEGKDEALAYVEERFTAHIAVR
QY	841 DVELJITGLDFYQDKVQPVSEBILQLKTYLPTFETTI
Db	841 DVELJITGLDFYQDKVQPVSEBILQLKTYLPTFETTI
	RESULT 2
	ADEB6103
	ID ADEB6103 standard; protein: 875 AA.
XX	XX
AC	ADEB6103;
XX	XX-2004 (first entry)

23-JAY-2004 FIRST EDITION						
Query Match 100.0%; Score 4804; DB 7; Length 875;	Best Local Similarity 100.0%; Pred. No. 0;	Mismatches 0; Indels 0; Gaps 0;		Human Protein AAC51813, SEQ ID NO 1944.	DE XX	
Matches 875; Conservative 0; Spared nerve injury; SNI; Chung.				Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.	KW KW KW KW XXX	
1 MESTIILATEQPVKNTLKKYKIACTIVLLAVIMSLGLIGLGKLRKLEKGSCRKICFD 60				Homo sapiens.	OS	
1 MESTIILATEQPVKNTLKKYKIACTIVLLAVIMSLGLIGLGKLRKLEKGSCRKICFD 60					PN PN	
61 ASFRGLENCRCDVACKDRGDCCWDFDTCEVESTIWMCNKFRCGCETRLASLSCSDCL 120				WO2003016475-A2.	XX	
61 ASFRGLENCRCDVACKDRGDCCWDFDTCEVESTIWMCNKFRCGCETRLASLSCSDCL 120					PD 27-FEB-2003.	
121 QKDCDCAKDKYKSVQCQGETSLEENCCTAQOQSQCPCGFDLPPVILPSM0GFAEYLTYWDTL 180				XX	PF 14-AUG-2002; 2002WO-US025765.	
121 QKDCDCAKDKYKSVQCQGETSLEENCCTAQOQSQCPCGFDLPPVILPSM0GFAEYLTYWDTL 180				XX	PR 14-AUG-2001; 2001US-0312147P.	
181 MPNINKLKLKG1HSKYMRAAMYPTKTFPNHYTIVTGLYPSPHGIIDNNNNYDVNLNKNEFLS 240				PR 01-NOV-2001; 2001US-0346389P.	PR 26-NOV-2001; 2001US-0333347P.	
181 MPNINKLKLKG1HSKYMRAAMYPTKTFPNHYTIVTGLYPSPHGIIDNNNNYDVNLNKNEFLS 240				XX	(GEHO) GEN HOSPITAL CORP.	
241 SKEQNPAWHQGPWMWLTAMYQGHKAATYFWPGSEVAINGSFPSIYMPNGSYFEEERIS 300				PA (FARB) BAYER AG.	PA	
241 SKEQNPAWHQGPWMWLTAMYQGHKAATYFWPGSEVAINGSFPSIYMPNGSYFEEERIS 300				XX	Woolf C, D'urso D, Beifort K, Costigan M;	
301 TLLKWLDPKAERPRFTYMYFEEDSSCHAGGPVSARYVKALQVVDHAFGMILEGKRN 360				XX	WPI; 2003-268312/26.	
301 TLLKWLDPKAERPRFTYMYFEEDSSCHAGGPVSARYVKALQVVDHAFGMILEGKRN 360				XX	DR GENBANK; AAC51813.	
361 LHNQVNIIILADHGMDQTNCRNEYMTDPRINFTYMEGAPRIRAHNIPHDFFFSNS 420				PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.	
361 LHNQVNIIILADHGMDQTNCRNEYMTDPRINFTYMEGAPRIRAHNIPHDFFFSNS 420				XX	Claim 1; Page; 1017pp; English.	
421 EETVRNLSRKPDQDFKPVLTPDLPKRLHYAKNRIDKWHLYDQQLWAVRSKSNNTNGCG 480				CC	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spiral segmental nerve injury (Chung). Chronic constriction	
421 EETVRNLSRKPDQDFKPVLTPDLPKRLHYAKNRIDKWHLYDQQLWAVRSKSNNTNGCG 480				CC	specification, pain or neuronal tissue), chronic constriction pain (e.g.,	
482 GHGYNNEFRSMEAIFLAQGPSPKEKTEVEPPFENIEYNLMDCLLRIOPAPNGTHGSLN 540				CC		
482 GHGYNNEFRSMEAIFLAQGPSPKEKTEVEPPFENIEYNLMDCLLRIOPAPNGTHGSLN 540				CC		
541 HLIKVPFYEPSSHAEVSKSVCGFANPLPTESDCFPHQNLSTOEQVNQNLJQEEI 600				CC		
541 HLIKVPFYEPSSHAEVSKSVCGFANPLPTESDCFPHQNLSTOEQVNQNLJQEEI 600				CC		
601 TATVKVNLFGRVRVQDNLKLYREYVSFGKAMRMPPMSYYTVQLQDTSPLPPT 660				CC		
601 TATVKVNLFGRVRVQDNLKLYREYVSFGKAMRMPPMSYYTVQLQDTSPLPPT 660				CC		
661 VPDCLRAVVPSESQKCSFYLADKNTRHGTYPAPPASRTSDQTDALITSNLVPMYE 720				CC		
661 VPDCLRAVVPSESQKCSFYLADKNTRHGTYPAPPASRTSDQTDALITSNLVPMYE 720				CC		

RESULT 3
ADE65891
ID ADE65891 standard; protein; 875 AA.
YY

Db	241. SKEONNPAAWHQGPWNKLTAMYQGLKAATYFWPGESEVAINGSPSPSIYMPNGSVPFPERIS	300	XX	A composition for diagnosing, preventing, and treating cancer (e.g. prostate, renal or uterine cancer) comprises 161P2F10B polymucleotides
Qy	301. TLLKWLDLKAERPRFTMYFEPPSSCHAGGPVSARVIKALQVVDHAFGMLMEGLKQRN	360	PT	
Qy	301. TLLKWLDLKAERPRFTMYFEPPSSCHAGGPVSARVIKALQVVDHAFGMLMEGLKQRN	360	PT	
Db	361. LANCVNIIILADHGMDCTYCNKMEYMTDFPRINFFMVEGAPTRAHNIPHDFFSNS	420	XX	Example 1; SEQ ID NO 16; 135pp; English.
Qy	361. LANCVNIIILADHGMDCTYCNKMEYMTDFPRINFFMVEGAPTRAHNIPHDFFSNS	420	XX	This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 1 protein of the invention.
Qy	422. EETVRNLSSRKPDGHFKRYLTPDPLRHLAYAKNRIDKXHFLFDQWMLARSKSNTNCGG	480	CC	
Db	422. EETVRNLSSRKPDGHFKRYLTPDPLRHLAYAKNRIDKXHFLFDQWMLARSKSNTNCGG	480	CC	
Qy	483. GNHGYNNFRSMAIFLAHGPSFKERTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN	540	CC	
Db	483. GNHGYNNFRSMAIFLAHGPSFKERTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN	540	CC	
Qy	541. HLLKVPFPEPSHAEVSKPSMAIFLAHGPSFKERTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN	600	CC	
Db	541. HLLKVPFPEPSHAEVSKPSMAIFLAHGPSFKERTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN	600	CC	
Qy	601. TATVKVNIFLGRGRVLQKQVDHLLYHPEYSGFGKAMMMSSTYVQLGDTSPRLPP	660	XX	Sequence 875 AA;
Db	601. TATVKVNIFLGRGRVLQKQVDHLLYHPEYSGFGKAMMMSSTYVQLGDTSPRLPP	660	XX	Query Match 100.0%; Score 4804; DB 7; Length 875;
Qy	661. VPDCLRADYRVPPSEQXCSFYLADKNITHGSLYPPASNRSQSDQYDALTSNLVPMYE	720	Qy	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Db	661. VPDCLRADYRVPPSEQXCSFYLADKNITHGSLYPPASNRSQSDQYDALTSNLVPMYE	720	Db	1 MESTLTLATEQPKVKTNLKKYKTAICVILLALIVIMSGLGLGLGLRLEKQGSCRKCFD 60
Qy	721. FROWDYFHSVLILKHATERNGNVWSGPPIFYDNYGHFADDEITKHLANTDVP1PTHY	780	Qy	1 MESTLTLATEQPKVKTNLKKYKTAICVILLALIVIMSGLGLGLRLEKQGSCRKCFD 60
Db	721. FROWDYFHSVLILKHATERNGNVWSGPPIFYDNYGHFADDEITKHLANTDVP1PTHY	780	Db	61 ASPFGLENRCRDYVACKDGRGCDWDFEPTCVCESTRIMCNKPFKGGETLEASICSCSDCL 120
Qy	781. FVVLTSCKNSHTPENCPCGWLDLPLF1PHRTNVVESCPGKPEALWVEERFTAHTAIVR	840	Qy	61 ASPFGLENRCRDYVACKDGRGCDWDFEPTCVCESTRIMCNKPFKGGETLEASICSCSDCL 120
Db	781. FVVLTSCKNSHTPENCPCGWLDLPLF1PHRTNVVESCPGKPEALWVEERFTAHTAIVR	840	Db	61 ASPFGLENRCRDYVACKDGRGCDWDFEPTCVCESTRIMCNKPFKGGETLEASICSCSDCL 120
Qy	841. DVEELLTGIDFYQDKVQPVSEIQLKTYLPTFETTI	875	Qy	121 QKDCDCADYKSVCOGETSWLEENCDAQSQSCPEGFLPPVILFMSMGFRAEYLYTMDTL 180
Db	841. DVEELLTGIDFYQDKVQPVSEIQLKTYLPTFETTI	875	Db	121 QKDCDCADYKSVCOGETSWLEENCDAQSQSCPEGFLPPVILFMSMGFRAEYLYTMDTL 180
Qy	841. DVEELLTGIDFYQDKVQPVSEIQLKTYLPTFETTI	875	Qy	181 MPNTINKLKTGIIISKPNAMYPTKTFPHHYTIVGLYPESHGJIDNNMYDVNLNKOFSL 240
Db	841. DVEELLTGIDFYQDKVQPVSEIQLKTYLPTFETTI	875	Db	181 MPNTINKLKTGIIISKPNAMYPTKTFPHHYTIVGLYPESHGJIDNNMYDVNLNKOFSL 240
Qy	RE SULT 4		Qy	301 TLWKWLDPKAERPRFTYTMYFEEPDSSCHAGGPVSARVIKALQVVDHAFGMLMEGLKQRN 360
ID	AD65904		Db	301 TLWKWLDPKAERPRFTYTMYFEEPDSSSHAGGPVSARVIKALQVVDHAFGMLMEGLKQRN 360
ID	ADE65904	standard; protein: 875 AA.	Db	241 SKEONNPAAWHQGPWNKLTAMYQGLKAATYFWGSESEVINGSPPSPSYMPNGSVPFERRIS 300
XX	XX		Db	241 SKEONNPAAWHQGPWNKLTAMYQGLKAATYFWGSESEVINGSPPSPSYMPNGSVPFERRIS 300
AC	ADE65904		Qy	361 LENCVNIIILADHGMDCTYCNKMEYMTDFPRINFFMVEGAPTRAHNIPHDFFSNS 420
DB	29-JAN-2004	(First entry)	Db	361 LENCVNIIILADHGMDCTYCNKMEYMTDFPRINFFMVEGAPTRAHNIPHDFFSNS 420
XX	XX		Qy	421 EETVRNLSSRKPKQHFPLYLTPDLPKELHYAQNVRIRKHLFVDQOMLAVRSKNTNCGG 480
DE	Human 161P2F10B protein variant 1 #2.		Db	421 EETVRNLSSRKPKQHFPLYLTPDLPKELHYAQNVRIRKHLFVDQOMLAVRSKNTNCGG 480
XX	XX		Qy	541 HLLKVPFPEPSHAEVSKPSFKEKTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN 540
XX	XX		Db	541 HLLKVPFPEPSHAEVSKPSFKEKTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN 540
XX	XX		Qy	541 HLLKVPFPEPSHAEVSKPSFKEKTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN 540
XX	XX		Db	541 HLLKVPFPEPSHAEVSKPSFKEKTEVEPPENIEVNLMEDLRIQAPANGNGTHGSLN 540
XX	XX		Qy	601 TATVKVNIFGFRPRVLOKNDVCLLYHREYYSGFGKAMRMPMWSSYVQLGDTSPPLPT 660
OS	Homo sapiens.		Db	601 TATVKVNIFGFRPRVLOKNDVCLLYHREYYSGFGKAMRMPMWSSYVQLGDTSPPLPT 660
XX	XX		Qy	661 VPDLRADYRVPPSEOKCSFYLADKITHGFLYPPASNRTSDSOYDALITSNLVPMYEE 720
PR	07-NOV-2001; 2001US-00005480.		Db	661 VPDLRADYRVPPSEOKCSFYLADKITHGFLYPPASNRTSDSOYDALITSNLVPMYEE 720
PR	31-JAN-2002; 2002US-00062109.		Qy	721 FRQWDYFHHSVLLKHATERNGNVWSGPPIFYDNYGHFADDEITKHLANTDVP1PTHY 780
XX	XX		DR	DR - PSDB; ADE65891.

Matches	875;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;		
QY	1	MESTLTLATEQPKKNTKKYKIACTIVLLVIMSLGLGLGKLEKGSCRKCFD	60							KW	161P2F10B; cancer; cytotoxic; gene therapy; vaccine; human.
Db	1	MESTLTLATEQPKKNTKKYKIACTIVLLVIMSLGLGLGKLEKGSCRKCFD	60							XX	
QY	61	ASFRGLENERCDVACKDRGDCCMDFEDTCVESTRMNKFRGEPLAEASLCSSCDDCL	120							OS	Homo sapiens.
Db	61	ASFRGLENERCDVACKDRGDCCMDFEDTCVESTRMNKFRGEPLAEASLCSSCDDCL	120							XX	
QY	121	QKDCCADYKSVCGETSWLEENCDTAGCOSQCEGFDLPPVILFSMDGFRAEYLTYWDTL	180							PD	15-MAY-2003.
Db	121	QKDCCADYKSVCGETSWLEENCDTAGCOSQCEGFDLPPVILFSMDGFRAEYLTYWDTL	180							XX	07-NOV-2002; 2002WO-US036002.
QY	181	MPNINKLKTCGTHSKYKRAMYPTKTFPHYTTVGLYPESHGIDDNMMYDNLKNFKSLS	240							PR	07-NOV-2001; 2001US-0005480.
Db	181	MPNINKLKTCGTHSKYKRAMYPTKTFPHYTTVGLYPESHGIDDNMMYDNLKNFKSLS	240							PR	31-JAN-2002; 2002US-00062109.
QY	241	SKEQNNPWAWHGQPMWLTAMYQSLKAATYFWPGSEVAINGSPPSIYMPYNGSVPFFERIS	300							XX	PA (AGEN-) AGENSY INC.
Db	241	SKEQNNPWAWHGQPMWLTAMYQSLKAATYFWPGSEVAINGSPPSIYMPYNGSVPFFERIS	300							XX	PI Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KJM;
QY	301	TLLKWLDPKAEEPRFYTMFEPDPSSHAGPVSARVTKALQVDFHAGMLMEGULKORN	360							PI	PI Morrison RK, Challita-Sid PM;
Db	301	TLLKWLDPKAEEPRFYTMFEPDPSSHAGPVSARVTKALQVDFHAGMLMEGULKORN	360							XX	XX WPI; 2003-441560/41.
QY	361	LHNCVNILLADIGMDQTYCNRMHEMTYFPRLNFYMEGAPRTRAHNTPHDFFSFNS	420							XX	Example 5; SEQ ID NO 94; 13pp; English.
Db	361	LHNCVNILLADIGMDQTYCNRMHEMTYFPRLNFYMEGAPRTRAHNTPHDFFSFNS	420							XX	A composition relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a diagnosis, the composition and methods of the invention are useful in a diagnosis, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 6 protein of the invention.
QY	421	EEIVRNLSRKPDQHFKYLTPDLPKRHYAKNRVIDXVHLFVDQWLAVERSKSNTNGG	480							XX	XX
Db	421	EEIVRNLSRKPDQHFKYLTPDLPKRHYAKNRVIDXVHLFVDQWLAVERSKSNTNGG	480							XX	XX
QY	481	GNTGYNNBRSMPEAIFIHLAHGSPSKEKTEVEPFENIEYNNLMDCLRIQAPANGTHGSLN	540							XX	XX
Db	481	GNHGYNNBRSMPEAIFIHLAHGSPSKEKTEVEPFENIEYNNLMDCLLRIQAPANGTHGSLN	540							XX	Sequence 875 AA;
QY	541	HLLKVPEYKPSHAEEVKPSVCGFANPLPTESLDCCFCHLQNSTOLEQVNQMLNLQEI	600							Query Match	100.0%; Score 4804; DB 7; Length 875;
Db	541	HLLKVPEYKPSHAEEVKPSVCGFANPLPTESLDCCFCHLQNSTOLEQVNQMLNLQEI	600							Best Local Similarity	100.0%; Prod. No. 0;
QY	601	TATVKVNLLFGPRVILQKWDHCLLYHEBYVSFGKAMRMPWMSYTVPQLGDTSPLPPT	660							Matches	0; Mismatches 0; Indels 0; Gaps 0;
Db	601	TATVKVNLLFGPRVILQKWDHCLLYHEBYVSFGKAMRMPWMSYTVPQLGDTSPLPPT	660							QY	1 MESTLTLATEQPKVNTLKKYKIACTIVLLVIMSLGIGLGLGKLRKLGQSCKRKCFD 60
QY	661	VPDCLLRADVPPRESEQCKCSFYLADKNTITHGFLYPAPSNTSDSQDALITSNLVPMEE	720							Db	1 MESTLTLATEQPKVNTLKKYKIACTIVLLVIMSLGIGLGLGKLRKLGQSCKRKCFD 60
Db	661	VPDCLLRADVPPRESEQCKCSFYLADKNTITHGFLYPAPSNTSDSQDALITSNLVPMEE	720							QY	61 ASFRGLENCRDVACKDRGDCCWDEDTCVESTRIMCNKFRGEPLTRLEASLCSDDCL 120
QY	721	FRKWDYFPHSVLLKHATERGNVNVSGPPIFDYNYDGHFDADEITKHLANTDVPIPTHY	780							Db	61 ASFRGLENCRDVACKDRGDCCWDEDTCVESTRIMCNKFRGEPLTRLEASLCSDDCL 120
Db	721	FRKWDYFPHSVLLKHATERGNVNVSGPPIFDYNYDGHFDADEITKHLANTDVPIPTHY	780							QY	121 QKDDCCADYKSVQCGETSMILEENCDAQQSQCPRGFDLPPVILPSMDGFRAEYLTYWDTL 180
QY	781	FVVLTSCKNKSHTPENCCGWLDPFPLPHRPNVNESSPEGPEALWVEERFTAIIARY	840							Db	121 QKDDCCADYKSVQCGETSMILEENCDAQQSQCPRGFDLPPVILPSMDGFRAEYLTYWDTL 180
Db	781	FVVLTSCKNKSHTPENCCGWLDPFPLPHRPNVNESSPEGPEALWVEERFTAIIARY	840							QY	121 SKEQQNPWAWHGQPMWLTAMYQGKAAATFWPGSESAVINGSFPSIYMPYNGSVPFEERLS 300
QY	841	DVELLTGDLDFYQDKVQPSSEIQLQKTTIPFTETI	875							Db	121 SKEQQNPWAWHGQPMWLTAMYQGKAAATFWPGSESAVINGSFPSIYMPYNGSVPFEERLS 300
Db	841	DVELLTGDLDFYQDKVQPSSEIQLQKTTIPFTETI	875							QY	181 MPNINKLKTCGTHSKYKRAMYPTKTFPHYTTVGLYPESHGIDDNMMYDNLKNFKSLS 240
QY	181	FVVLTSCKNKSHTPENCCGWLDPFPLPHRPNVNESSPEGPEALWVEERFTAIIARY	840							Db	181 MPNINKLKTCGTHSKYKRAMYPTKTFPHYTTVGLYPESHGIDDNMMYDNLKNFKSLS 240
QY	241	RESULT 8								QY	181 SKEQQNPWAWHGQPMWLTAMYQGKAAATFWPGSESAVINGSFPSIYMPYNGSVPFEERLS 300
1D	ADE65982	standard; protein; 875 AA.								Db	241 SKEQQNPWAWHGQPMWLTAMYQGKAAATFWPGSESAVINGSFPSIYMPYNGSVPFEERLS 300
XX										QY	301 TLLKWLDPKAEEPRFYTMFEPDPSSHAGPVSARVTKALQVDFHAGMLMEGULKORN 360
AC										Db	301 TLLKWLDPKAEEPRFYTMFEPDPSSHAGPVSARVTKALQVDFHAGMLMEGULKORN 360
XX										QY	361 LHNCVNILLADIGMDQTYCNRMHEMTYFPRLNFYMEGAPRTRAHNIPHDFFSFNS 420
DT										Db	361 LHNCVNILLADIGMDQTYCNRMHEMTYFPRLNFYMEGAPRTRAHNIPHDFFSFNS 420
XX										QY	421 BEIVNLSCRPDKQFFKPYLTPDKEKRLHYAKNRYIDKTHLFYDQWLAVERSKSNTNGC 480
DE										XX	Human 161P2F10B protein variant 6 #2.

RESULT 9
 ADE65909
 IID ADE65909 standard; protein; 875 AA.
 XXX
 ADE65909;
 ACAC
 XXX
 DDT
 XXX
 DEDE
 XXX
 KWKW
 XXX
 OSOS
 XXX
 PNPN
 XXX
 PDPD
 XXX
 Homo sapiens.
 (first entry)
 Human 161P2F10B protein variant 1 #3.
 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human;
 WO2003040340-A2.
 15-MAY-2003.

07 NOV 2002, 2002NS 00000002;
XXX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
(AGEN-) AGENSYS INC.
XXX Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison RK, Challita-Hid PM, Morrison RK,

DR XXX
WPI; 2003-441560/41.
A composition for diagnosing, preventing and treating cancer (e.g. prostatic, renal or uterine cancer) comprises 161B2F10B polynucleotides and polypeptides.

XX
Example 2; SEQ ID NO 21; 135PP; English.

XX
This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161B2F10B), and its variants having a sequence of 85 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161B2F10B protein, and the gene which encodes it, may be useful

C for gene therapy or the development of a vaccine. The composition and
C methods of the invention are useful in diagnosing, preventing and
C treating cancer. The present sequence is the amino acid sequence of the
C human 161P2F10B variant 1 protein of the invention.

Query Match	Score	DB 7:	Length	875:
Best Local Similarity	100.0% Matches 875	Pred. No. 0; Conservative 0;	0;	Gaps 0;
y	1	MESTIITLATEQPKYKNTLKKYKTA CIVILIAVIMSLGIGIGRKL EKQGSCRKCFD 60		
b	1	MESTIITLATEQPKYKNTLKKYKTA CIVILIAVIMSLGIGIGRKL EKQGSCRKCFD 60		
y	61	ASPRGLENCRDYACKDGCMDPE DTCVESTRIMCNKFRGE TRLEASICSCDDCL 120		
b	61	ASPRGLENCRDYACKDGCMDPE DTCVESTRIMCNKFRGE TRLEASICSCDDCL 120		
y	121	QRKD CADYKSVCOGETSWLE ENCDTAQSQCPEGFD- PPVILEFSMDGFRAYLY TDTL 180		
b	121	QRKD CADYKSVCOGETSWLE ENCDTAQSQCPEGFD- PPVILEFSMDGFRAYLY TDTL 180		
y	181	MPNINLKLTGIGHSKYM EAMYPTKTFP HYTIVTGHYPE SHGQIIDNMMYD VNLNKNSFLS 240		
b	181	MPNINLKLTGIGHSKYM EAMYPTKTFP HYTIVTGHYPE SHGQIIDNMMYD VNLNKNSFLS 240		
y	241	SKEQNPNPAWHGQPMWLTAMY QCLKAATYFWPGSE VAINGSPSI MPYNGSVP PERIS 300		
b	241	SKEQNPNPAWHGQPMWLTAMY QCLKAATYFWPGSE VAINGSPSI MPYNGSVP PERIS 300		
y	301	TLLKMDLPKAERPRF YFTMYFEEDSS CHAGGEVS ARVYI KALQV DHA FGMLME GKRN 360		
b	301	TLLKMDLPKAERPRF YFTMYFEEDSS CHAGGEVS ARVYI KALQV DHA FGMLME GKRN 360		
y	361	LHNCVNTILLADHCM DQTYCNKMEY MTDYP RINFYME EGPAPR RAHNTP HDFFSFNS 420		
b	361	LHNCVNTILLADHCM DQTYCNKMEY MTDYP RINFYME EGPAPR RAHNTP HDFFSFNS 420		
y	421	EETVRNLSCRKP DOHF KPYLTDPD PKRLHYA KNV RTDKVH FVDQ QWLAV RSK NSNT NGCG 480		
b	421	EETVRNLSCRKP DOHF KPYLTDPD PKRLHYA KNV RTDKVH FVDQ QWLAV RSK NSNT NGCG 480		
y	481	GNHGYNNERSM EAFLAHG PSKKE VEP FEN IEN YLN MDL RQ PAP NNG TGS LSN 540		
b	481	GNHGYNNERSM EAFLAHG PSKKE VEP FEN IEN YLN MDL RQ PAP NNG TGS LSN 540		
y	541	HLLKV PFYEP PSHA EVSK FSV CG FAN PL PTE LSDC FC PHL QNST OLE QV NQ ML NL QE EI 600		
b	541	HLLKV PFYEP PSHA EVSK FSV CG FAN PL PTE LSDC FC PHL QNST OLE QV NQ ML NL QE EI 600		
y	601	TATKV NL PFG GR PRL QX V L K H A T E R G Y N V S C P I D Y N D H F A D P E I T K H L A N T D V P I T H Y 780		
b	601	TATKV NL PFG GR PRL QX V L K H A T E R G Y N V S C P I D Y N D H F A D P E I T K H L A N T D V P I T H Y 780		
y	661	VPDCL RADY RV P S E Q K CS F Y L A D R N T H G L Y P A S N R T S D Q D A L I T S N L V P N Y E 720		
b	661	VPDCL RADY RV P S E Q K CS F Y L A D R N T H G L Y P A S N R T S D Q D A L I T S N L V P N Y E 720		
y	721	FRKWDY FHS VLL K H A T E R G Y N V S C P I D Y N D H F A D P E I T K H L A N T D V P I T H Y 780		
b	721	FRKWDY FHS VLL K H A T E R G Y N V S C P I D Y N D H F A D P E I T K H L A N T D V P I T H Y 780		
y	781	FVVLTSCK KNK SHT PEN CP GWL DVL P F I P H R P T N V S C P E G X P E A L W E E R T H A I A R V R 840		
b	781	FVVLTSCK KNK SHT PEN CP GWL DVL P F I P H R P T N V S C P E G X P E A L W E E R T H A I A R V R 840		
y	841	DVELT GTG D F Y Q D K V P Y S E L L Q K T L P T F E T I 875		
b	841	DVELT GTG D F Y Q D K V P Y S E L L Q K T L P T F E T I 875		

RESULT 10

XX	XX	XX	XX	XX	Db	781	FVVLTSCKNSHTPENCPGWLDPFTIPHRPTNVECPGKPEALWVEERFTAHIARVR	840
PS Disclosure; Fig 13A; 135pp; English.					QY	841	DVELLTGIDFYQDKVQPSSEILQLKTYLPLTFETTI	875
This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 1 protein of the invention.					Db	841	DVELLTGIDFYQDKVQPSSEILQLKTYLPLTFETTI	875
XX	Sequence 875 AA;	Query Match 100.0%; Score 4804; DB 7; Length 875;	Best Local Similarity 100.0%; Pred. No. 0;	Mismatches 0;	Db	161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.		
Matches 875; Conservative 0; Indels 0; Gaps 0;			XX	XX	QY	1	MESTLTLATEQPVKNTLKRYKIACTVLALLIVMSIGLGLGIRKLEKGSCRKKCFD	60
Db	1	MESTLTLATEQPVKNTLKRYKIACTVLALLIVMSIGLGLGIRKLEKGSCRKKCFD	60	OS Homo sapiens.	Db	W02003040340-A2.		
QY	61	ASPRGLENCORDVACKORGDCWDFFDTCVESTRIMCNKERCGETRLAESLICSCSDDCL	120	XX	QY	15-MAY-2003.		
Db	61	ASPRGLENCORDVACKORGDCWDFFDTCVESTRIMCNKERCGETRLAESLICSCSDDCL	120	XX	Db	07-NOV-2002; 2002WO-US036002.		
QY	121	QKDCCADIKSYKSYCQGETSWLNECDTAQQSQCEPGLLPVILFSMDGFAEYLWTDL	180	XX	QY	07-NOV-2001; 2001US-00005180.		
Db	121	QKDCCADIKSYKSYCQGETSWLNECDTAQQSQCEPGLLPVILFSMDGFAEYLWTDL	180	XX	Db	31-JAN-2002; 2002US-00062109.		
QY	181	MPNINKLKTGTHSKTKYRAMYPTKTFKNHNYTIVGPESHGIDDNMYDNLNKNSLS	240	XX	QY	PA (AGEN-) AGENSYS INC.		
Db	181	MPNINKLKTGTHSKTKYRAMYPTKTFKNHNYTIVGPESHGIDDNMYDNLNKNSLS	240	XX	Db	Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;		
QY	241	SKEQNNPAPWHGPWMILTAMYOGLKATYFWGSEVAINGSFPSIYMPNGSVPFEEIRS	300	XX	Db	Morrison RK, Challita-Bid PM;		
Db	241	SKEQNNPAPWHGPWMILTAMYOGLKATYFWGSEVAINGSFPSIYMPNGSVPFEEIRS	300	XX	QY	WPI; 2003-441560/41.		
QY	301	TUJKWLDLPKAKSPRFETMYFREPDSGGHAGCPVPSARVITALQVYDHAFCMUMELBKQNL	360	XX	QY	A composition for diagnosing, preventing and treating cancer (e.g. prostate, renal or uterine cancer) comprises 161P2F10B polynucleotides and polypeptides.		
Db	301	TUJKWLDLPKAKSPRFETMYFREPDSGGHAGCPVPSARVITALQVYDHAFCMUMELBKQNL	360	XX	Db	Example 2; SEQ ID NO 22; 135pp; English.		
QY	361	LANCVNITLADHGMDTYCNRMEMYMTDFPRINFEYMMEGPAPRIRANNIPHDEFSNS	420	XX	Db	CC This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B K122R variant protein which was used for homology purposes and is related to the invention.		
Db	361	LANCVNITLADHGMDTYCNRMEMYMTDFPRINFEYMMEGPAPRIRANNIPHDEFSNS	420	XX	QY	XX		
QY	421	EEIVRNLSCKRDQHFPPYLDPLPKRLHYAKNRVIDKVLFLFDQWLAIRSKSNTNCGG	480	CC	Db	CC		
Db	421	EEIVRNLSCKRDQHFPPYLDPLPKRLHYAKNRVIDKVLFLFDQWLAIRSKSNTNCGG	480	CC	QY	CC		
QY	481	GNGYNNFRSMEAIFIAGHPSPKEKEPEPENTEVNNNCDLRIQPAFPNNGTHGSLN	540	CC	Db	CC		
Db	481	GNGYNNFRSMEAIFIAGHPSPKEKEPEPENTEVNNNCDLRIQPAFPNNGTHGSLN	540	CC	QY	CC		
QY	541	HLLKVPPYEPSSHAEEVSKFSYCGFANPLPTESLCFCPHLONSTOLEQVQMLNLTQET	600	CC	Db	CC		
Db	541	HLLKVPPYEPSSHAEEVSKFSYCGFANPLPTESLCFCPHLONSTOLEQVQMLNLTQET	600	CC	QY	CC		
QY	601	TATVKVNLPGFPRVPLQKNDVHDCLHYREYYVSFGKAMRMEMWSSYTPOLGDTSPLPT	660	DB	1 MESTLTLATEQPVKNTLKRYKIACTVLALLIVMSIGLGLGIRKLEKGSCRKKCFD	60		
Db	601	TATVKVNLPGFPRVPLQKNDVHDCLHYREYYVSFGKAMRMEMWSSYTPOLGDTSPLPT	660	QY	1 MESTLTLATEQPVKNTLKRYKIACTVLALLIVMSIGLGLGIRKLEKGSCRKKCFD	60		
QY	661	VPDCLRAVDVYPVPSSEQKCSKPSYLAQKNTTGFLYPASNTSDQYDALITSNLYPMYE	720	DB	1 MESTLTLATEQPVKNTLKRYKIACTVLALLIVMSIGLGLGIRKLEKGSCRKKCFD	60		
Db	661	VPDCLRAVDVYPVPSSEQKCSKPSYLAQKNTTGFLYPASNTSDQYDALITSNLYPMYE	720	QY	61 ASPRGLENCRCDFACKORGDCWDFFDTCVESTRIMCNKFRGEGTRLEASLCSDDCL	120		
QY	721	FRKQWDFHSVSLLIKATERGVNVYVSGPISPDYNQDGHPADPETKHLNTDVPIPHY	780	Db	61 ASPRGLENCRCDFACKORGDCWDFFDTCVESTRIMCNKFRGEGTRLEASLCSDDCL	120		
Db	721	FRKQWDFHSVSLLIKATERGVNVYVSGPISPDYNQDGHPADPETKHLNTDVPIPHY	780	QY	121 OKDCCADYKSYCQGETSWLBENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLWTDL	180		
QY	781	FVVLTSCKNSHTPENCPGWLDPFTIPHRPTNYESCPGKPEALWVEERFTAHIARVR	840	Db	121 QRDCCADYKSYCQGETSWLBENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLWTDL	180		

Db	601 TATVKVNLPFFGRPRVLRQKVDHCLLYHREYVSGFGKAVMMPMNSSTVPLQGDTSP1PPT	60	Qy	1 MESTLILATEQPKRKTTLKRYKIACTIVLALLVIMSIGIIGLGLRLRKEQGSCKRKCFD	60
Qy	661 VPDCLRADYRVPPSESQKCSFLADKNITHGFLYPPASNRTPSDQYDALITSNLPVPTEE	720	Db	1 MESTLILATEQPKRKTTLKRYKIACTIVLALLVIMSIGIIGLGLRLRKEQGSCKRKCFD	60
Db	661 VPDCLRADYRVPPSESQKCSFLADKNITHGFLYPPASNRTPSDQYDALITSNLPVPTEE	720	Qy	61 ASFRGLENCRCDVACKDRGDCWDFDTCEVESTRIMCNKFRCGTTRLEASLCSDDCL	120
Qy	721 FRRQWDYFPISSVLILKHATERNGNVVSGTIFDNYDGHFADAPBITHKLANTDVP1PHTY	780	Db	61 ASFRGLENCRCDVACKDRGDCWDFDTCEVESTRIMCNKFRCGTTRLEASLCSDDCL	120
Db	721 FRRQWDYFPISSVLILKHATERNGNVVSGTIFDNYDGHFADAPBITHKLANTDVP1PHTY	780	Qy	62 QKDCDCAKDYKSVQCGETSWSLEENCDTAQQSQCPEGFDLPPVTFSMQDFRAEYLTYDFTL	180
Qy	781 FVVLTSCKRKSHTPENCPGWLDVLPFLIPHRPTNVECPEGKPEALWVEERFTAHTARVR	840	Db	62 QKDCDCAKDYKSVQCGETSWSLEENCDTAQQSQCPEGFDLPPVTFSMQDFRAEYLTYDFTL	180
Db	781 FVVLTSCKRKSHTPENCPGWLDVLPFLIPHRPTNVECPEGKPEALWVEERFTAHTARVR	840	Qy	181 MPNTINKLKTGCGTHSKYMRAMYPKTFPHHYTITGLYBBSHGTLIDNNMYDVLNKNSLS	240
Qy	841 DVELLTGFLDFYQDKVQPVSEIOLQKTYLPFTETTI	875	Db	181 MPNINRKLKTGCGTHSKYMRAMYPKTFPHHYTITGLYBBSHGTLIDNNMYDVLNKNSLS	240
Db	841 DVELLTGFLDFYQDKVQPVSEIOLQKTYLPFTETTI	875	Qy	241 SKEQNPNPAWHGQPMWLAMYQGKLAARYFWPSSEVAINGSPS1IIMPYNGSYPFEBRIS	300
Db	RESLT 14		Db	241 SKEQNPNPAWHGQPMWLAMYQGKLAARYFWPSSEVAINGSPS1IIMPYNGSYPFEBRIS	300
ADB65893			Qy	301 TLWKWLDPKAERPRFTMYFEEDSSHAGGPVSARVTKALQVVDHAFGMLMEGLQRN	360
ID	ADB65893 standard; protein;	875 AA.	Db	301 TLWKWLDPKAERPRFTMYFEEDSSHAGGPVSARVTKALQVVDHAFGMLMEGLQRN	360
XX			Qy	361 LHNCVNLILLADHGMDQTYCNCNEMYMTDFPRINFFYEGPAPRIRAHN1PHDFFEFNS	420
AC			Db	361 LHNCVNLILLADHGMDQTYCNCNEMYMTDFPRINFFYEGPAPRIRAHN1PHDFFEFNS	420
XX			Qy	421 EETIVRNLSCKRKDQHFKPFLTPDLPKLAHAYNVRIDKVHLFYDQOWLAYRSKSNTNCGG	480
DT	29-JAN-2004 (first entry)		Db	421 EETIVRNLSCKRKDQHFKPFLTPDLPKLAHAYNVRIDKVHLFYDQOWLAYRSKSNTNCGG	480
XX			Qy	481 GHGYNNEFRMSMEAIAFLAHGSPFKEKTEVEPENENIVYLNCDLIRIOPAPNNGTHGSLN	540
DE	Human 161P2F10B protein variant 2.		Db	481 GHGYNNEFRMSMEAIAFLAHGSPFKEKTEVEPENENIVYLNCDLIRIOPAPNNGTHGSLN	540
XX			Qy	541 HLLKVPYEPSPHAEEVSKFVCGFANFLPTEELDCCPHLONSTOLEQVQNMNLNTQEELI	600
KW	161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.		Db	541 HLLKVPYEPSPHAEEVSKFVCGFANFLPTEELDCCPHLONSTOLEQVQNMNLNTQEELI	600
XX			Qy	601 TATVKVNLPFGSPRVTQXNDVCLLYHREYVSGFGKAMRMWMSSTVPLQGDTSP1PPT	660
OS	Homo sapiens.		Db	601 TATVKVNLPFGSPRVTQXNDVCLLYHREYVSGFGKAMRMWMSSTVPLQGDTSP1PPT	660
XX			Qy	661 VPDCLRADVRVPPSESQKCSFLADKNTITGFLYPPASNRTSQDYLALTSNLYPMYEE	720
FN	WO2003040340-A2.		Db	661 VPDCLRADVRVPPSESQKCSFLADKNTITGFLYPPASNRTSQDYLALTSNLYPMYEE	720
XX			Qy	721 FRKMDYFHVSVLLIKEATERNGVNTVSGPFDYNYDGHFDAPDEITKHLANTDVP1PHTY	780
PD	15-MAY-2003.		Db	721 FRKMDYFHVSVLLIKEATERGVNVVSGPFDYNYDGHFDAPDEITKHLANTDVP1PHTY	780
XX			Qy	781 FVVLTSCKRKSHTPENCPGNLDVLPFIIPHRTPTNVECPEGKPEALWVEERTAHARVR	840
PP	07-NOV-2002; 2002WO-US0360002.		Db	781 FVVLTSCKRKSHTPENCPGNLDVLPFIIPHRTPTNVECPEGKPEALWVEERTAHARVR	840
XX			Qy	841 DVELLTGFLDFYQDKVQPVSEIOLQKTYLPFTETTI	875
PR	07-NOV-2001; 2001US-00005480.		Db	841 DVELLTGFLDFYQDKVQPVSEIOLQKTYLPFTETTI	875
PR	31-JAN-2002; 2002US-00062109.		Qy	841 DVELLTGFLDFYQDKVQPVSEIOLQKTYLPFTETTI	875
XX			Db	841 DVELLTGFLDFYQDKVQPVSEIOLQKTYLPFTETTI	875
(AGEN -) AGENSYS INC.			Qy	RESULT 15	
XX			Db	XX	
Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;			Qy	XX	
PJ	Morrison RK, Chalilta-Eid PM;		Db	XX	
WPI; 2003-441560/41.			Qy	XX	
DR	N-PSDB; ADB65892.		Db	XX	
XX			Qy	XX	
A composition for diagnosing, preventing and treating cancer (e.g. prostatic, renal or uterine cancer) comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 2 protein of the invention.					
XX			CC	Sequence 875 AA;	
XX			CC	Query Match 99.9%; Score 4801; DB 7; Length 875;	
XX			CC	Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Gaps 0;	
XX			CC	Matches 874; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
XX			CC	Human 161P2F10B protein variant 4.	
XX			CC	161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.	
SQ			XX	Sequence 875 AA;	
			XX	29-JAN-2004 (first entry)	

OS Homo sapiens.
 XX WO2003040340-A2.
 XX PD 15-MAY-2003.
 XX PF 07-NOV-2002; 2002WO-US036002.
 XX PR 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX PA (AGEN-) AGENSY INC.
 XX PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;
 PI Morrison RK, Chaillita-Eid PM;
 XX DR WPI; 2003-441560/41.
 DR N-PSDD; AD65896.
 XX PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX PS Claim 1; SEQ ID NO 9; 135PP; English.
 XX CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel protein (161P2F10B) and its variants
 CC having a sequence of 875 amino acids provided in the specification. The
 CC protein of the invention may have cytostatic activity and the sequence
 CC compounds of the invention may be over-expressed in certain cancers. The
 CC sequence of the 161P2F10B protein, and the gene which encodes it, may be useful
 CC for gene therapy or the development of a vaccine. The composition and
 CC methods of the invention are useful in diagnosing, preventing and
 CC treating cancer. The present sequence is the amino acid sequence of the
 CC human 161P2F10B variant 4 protein of the invention.
 XX SQ Sequence 875 AA;

Query Match 99.9%; Score 4798; DB 7; Length 875;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 874; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESTLTLATEQPYKNTLKKYKIACTIVLLALIVMSIGLGLGLGRKLKEQGSCREKCFD 60
 DB 1 MESTLTLATEQPYKNTLKKYKIACTIVLLALIVMSIGLGLGLGRKLKEQGSCREKCFD 60

QY 61 ASPLGLENCBCDVACKGDCCWDRENTCVESTRIMONKFCGETRLAESLCSCSDDCL 120
 DB 61 ASPLGLENCBCDVACKGDCCWDRENTCVESTRIMONKFCGETRLAESLCSCSDDCL 120

QY 121 QKDCCADAKYSVCGETSMLEENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180
 DB 121 QKDCCADAKYSVCGETSMLEENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180

QY 181 MPNINKLKGIGHSKYMAMYPTKTFPNHYITVTGLYFESHLIDDNMMYDNLNKFLS 240
 DB 181 MPNINKLKGIGHSKYMAMYPTKTFPNHYITVTGLYFESHLIDDNMMYDNLNKFLS 240

QY 241 SKEONNPAAWHGOPNWLTAMYOGIKAATYFWPGESEAVINGSFFPSIYMPYNGSVPFEBRIS 300
 DB 241 SKEONNPAAWHGOPNWLTAMYOGIKAATYFWPGESEAVINGSFFPSIYMPYNGSVPFEBRIS 300

QY 301 TLKWLDPKAERPRFYTMYFEEDPSGHAGGPVSARTIKALQYDHFQWMAVRSKSNTNGG 360
 DB 301 TLKWLDPKAERPRFYTMYFEEDPSGHAGGPVSARTIKALQYDHFQWMAVRSKSNTNGG 360

QY 361 LHNCVNILLADHGMDQTYCNKMEYMTDYPFRINFFYMYEGPAPRIRAHNIHDFEFSNS 420
 DB 361 LHNCVNILLADHGMDQTYCNKMEYMTDYPFRINFFYMYEGPAPRIRAHNIHDFEFSNS 420

QY 421 EEEVNLSCERPKDQHFKPYLTPDLPKRYLEYAKNRVIDKYLFDQWMAVRSKSNTNGG 480
 DB 421 EEEVNLSCERPKDQHFKPYLTPDLPKRYLEYAKNRVIDKYLFDQWMAVRSKSNTNGG 480

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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:17:02 ; Search time 23 Seconds
(without alignments)

Title: US-10-005-480A-743

Perfect score: 4804

Sequence: 1 MESTILATEQPVKENTLKK.....QPVSEILQLKTYLPFTETTI 875

Scoring table: BLOSUM62

Gapop: 10.0 , Gapext 0.5

Searched: 388414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:
 1: /cgcn2_6.ptodata/2/iaaa/5A_COMB.pep:
 2: /cgcn2_6.ptodata/2/iaaa/5B_COMB.pep:
 3: /cgcn2_6.ptodata/2/iaaa/6A_COMB.pep:
 4: /cgcn2_6.ptodata/2/iaaa/6B_COMB.pep:
 5: /cgcn2_6.ptodata/2/iaaa/PECTUS_COMB.pep:
 6: /cgcn2_6.ptodata/2/iaaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	2498.5	52.0	873	3 US-09-187-331-6	Sequence 6, Appli	
2	2498.5	52.0	873	4 US-09-470-946-6	Sequence 6, Appli	
3	2498.5	52.0	873	4 US-09-438-906-2	Sequence 2, Appli	
4	2498.5	52.0	925	2 US-08-392-946-1	Sequence 1, Appli	
5	2498.5	52.0	925	2 US-08-501-169-1	Sequence 1, Appli	
6	2498.5	52.0	900	1 PCT-US94-14893-1	Sequence 1, Appli	
7	2494.5	51.9	873	4 US-09-438-906-4	Sequence 4, Appli	
8	2040.5	42.5	915	1 US-08-346-455B-69	Sequence 69, Appli	
9	10	2040.5	42.5	915	4 US-01-977-221-69	Sequence 69, Appli
10	2040.5	42.5	915	4 US-09-483-831B-34	Sequence 69, Appli	
11	2040.5	42.5	915	5 PCT-US95-06613-69	Sequence 69, Appli	
12	1964.5	40.9	829	3 US-08-346-455B-34	Sequence 34, Appli	
13	1964.5	40.9	829	3 US-08-977-221-34	Sequence 34, Appli	
14	1964.5	40.9	829	4 US-09-483-831B-34	Sequence 34, Appli	
15	1964.5	40.9	829	5 PCT-US95-06613-34	Sequence 34, Appli	
16	1923.5	40.0	861	1 US-08-346-455B-67	Sequence 67, Appli	
17	1923.5	40.0	861	3 US-08-977-221-67	Sequence 67, Appli	
18	1923.5	40.0	861	4 US-09-483-831B-67	Sequence 67, Appli	
19	1923.5	40.0	861	5 PCT-US95-06613-67	Sequence 67, Appli	
20	1838.5	38.3	979	1 US-08-346-455B-38	Sequence 38, Appli	
21	1838.5	38.3	979	3 US-08-977-221-38	Sequence 38, Appli	
22	1838.5	38.3	979	4 US-09-483-831B-70	Sequence 70, Appli	
23	1838.5	38.3	979	5 PCT-US95-06613-38	Sequence 38, Appli	
24	1761.5	36.7	788	1 US-08-346-455B-36	Sequence 36, Appli	
25	1761.5	36.7	788	3 US-08-977-221-36	Sequence 36, Appli	
26	1761.5	36.7	788	4 US-09-483-831B-36	Sequence 36, Appli	
27	1761.5	36.7	788	5 PCT-US95-06613-36	Sequence 36, Appli	

ALIGNMENTS

RESULT 1
US-09-187-331-6
; Sequence 6, Application US-09187331
; GENERAL INFORMATION.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Karl C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
; FILE REFERENCE: PF-0631.US
; CURRENT APPLICATION NUMBER: US-09/187-331
; SEQ ID NO: 6
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: g189650
US-09-187-331-6

Query Match 52.0% ; Score 2498.5 ; DB 3 ; Length 873;
Best Local Similarity 53.1% ; Pred. No. 8-235;
Matches 465 ; Conservative 137 ; Mismatches 250 ; Indels 23 ; Gaps 11;

QY 10 EQPVKK---NTLK--KYKACIVSALLVIMSIGLGLIGRLKLEQGSCRKKCFCFDAS 62
Db 5 EEPPEAKRARTAPDNTYKVLSLVSVCVITLUCIFGKPKPSAKEYKSCKGRFERT 64

QY 11 EPPPEAKRARTAPDNTYKVLSLVSVCVITLUCIFGKPKPSAKEYKSCKGRFERT 64

QY 12 5DCCINTSSVCQGEKSNVEEPCSTINEPQCPAGFETPTPLFSLJGFRABYLHTWGGLLP 181

QY 13 NTIKLKGTCIHKSKYMRAMYPIKTFPNHYTIVTGLYFESHLIDNNYYDNLNKFSLSSK 122

Db 65 F---GNRCRDAACVELNCCLDYQETCIEPHWINTCNKFICGEKLTRSLCACSDCRDK 121

QY 14 1DKNYDPKRNASFSLSK 123

QY 15 KODCADYKSVQCGETSMILEENCDTAQSQCPREGEDLPPVLFPSMUGFRAYLYTDIMP 182

Db 16 GDCCINTSSVCQGEKSNVEEPCSTINEPQCPAGFETPTPLFSLJGFRABYLHTWGGLLP 181

QY 17 1DKNYDPKRNASFSLSK 183

QY 18 1DKNYDPKRNASFSLSK 242

Db 19 1DKNYDPKRNASFSLSK 182

QY 20 1DKNYDPKRNASFSLSK 241

QY 21 1DKNYDPKRNASFSLSK 241

QY 22 1DKNYDPKRNASFSLSK 243

QY 23 1DKNYDPKRNASFSLSK 302

Db 24 1DKNYDPKRNASFSLSK 242

QY 25 1DKNYDPKRNASFSLSK 301

QY 26 1DKNYDPKRNASFSLSK 362

Db	3.02	LQWLCLPDKDERPHFVTLIYEPDSSGSHSYGPVSSEVIKALQRVDGVMGLMDGLKEKLNLH	361
Qy	3.63	NCVNITILLADHGMDQTYCNKMEYNTDFPRINFFYMYEGPAPTRAHNIPHDEFSFNSEE	422
Db	3.62	RCLNLLISDHGMEMEQGSCKRYIVLNKYLGDVKNTVKVTPAARLPSDVPDKYSFNVEG	421
Qy	4.23	IVRNLNSCRKPQDFPKPYLTPLKPLRHYAKNVRIDKVLFDQW-LAVRSKENTNCGG	481
Db	4.22	IARNLNSCERNQHDFPKPYLKHLFLPRLPAKSDRLEPLTFYLDQWQLANPSPKYGSG	481
Qy	4.82	NHGYNNEFRSMEALLFLANGPSFKERTEVEPKFENIPEVNLCDLRLQAPANNTHGSLNH	541
Db	4.82	FHGSDDNFVNMQALFGVGPGRFHKGIEADTFENIEVNLMCDLNLTAPEHNGTHGSLNH	541
Qy	54.2	LLKVPFYBRSAAEVSKFESVCGFPANPLTESLDCFC-PHLQNSTOLEQVNOMNLNLTQEBI	600
Db	54.2	LLXNPVTPKHPKREWHPLVQCPFTN-PRDNLCSCNPSI---LP1EDFQTOPENLYVAE	597
Qy	60.1	TATVKVNIPFGRPEPVLFQVNDHCLLIREYVSDFGKAMRMPKMSSTYVPOLDTSPIRPT	660
Db	59.8	KIKHETLDPYGRPVALQENTICLLSQHQFMSYQSQDLIMPWTSXTVDR-NDSFSTED	655
Qy	65.1	VPDCLRADPVRVPPSESEQCSFYLADKNTITHGFYLPASNRRTSDQY-DALITSNLVYME	719
Db	65.6	FSICLYQDFRIPUSPVHCSFTZNNKTVSYGFLSPQLNKNSG1SEBALLTNTVPMYQ	715
Qy	72.0	BFRKMDYFHSVLLIKHATERGVNTVSGPIFDYNTDGHFDADDEITKH--LANTDVPI	776
Db	71.6	SFWRWYFHDTLRKYAEERGVNTVSGPVDFDVGRCOSLENLRQKRRVIRNQEILI	775
Qy	77.7	PTHYFWLTSCKNSKSHPENCGWLDLPLF1PFRPNVESPEGIPEALVVEERTAHI	836
Db	77.6	PTHFFVLTWSCKDTSQPLHCCN-LDTLAFILPHRTNTNSECVGHHDSSWTEILLMLHR	834
Qy	83.7	AERVDRVEELTGIDFYQDKVQPVSEIILOKTYLPTF	871
Db	83.5	ARTDVEHITGFSYQSRKPEVSDILXKTHLPTF	869
RESULT 2			
US -09-470-946-6			
; Sequence 6 , Application US/09470946			
; Patent No. 6558923			
; GENERAL INFORMATION:			
; APPLICANT: Rue, Henry			
; APPLICANT: Corley, Neil C.			
; APPLICANT: Guegler, Karl J.			
; APPLICANT: Gorgone, Gina A.			
; APPLICANT: Baughn, Mariah R.			
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS			
; FILE REFERENCE: EP-0631 US			
; CURRENT APPLICATION NUMBER: US/09/470,946			
; CURRENT FILING DATE: 1999-12-22			
; EARLIER APPLICATION NUMBER: US 09/187,331			
; EARLIER FILING DATE: 1998-11-06			
; NUMBER OF SEQ ID NOS: 6			
; SEQ ID NO 6			
; LENGTH: 873			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE: -			
; OTHER INFORMATION: 9189650			
US -09-470-946-6			
Query Match 52.0% ; Score 2498.5 ; DB 4 ; Length 873;			
Best Local Similarity 53.1% ; Pred. No. 8e-215 ; Mismatches 250 ; Indels 23 ; Gaps 11;			
Matches 463 ; Conservative 137 ;			
10 EQPVTKK---NTLK---KYKACIYVLLAVIMSIGGGLGLRKLEKOGSCRKCFDAS 62			
5 EEPPLKAARTAKDPTYKVLSSVCPVTTLGICLKPSSAKEYSKCGRCPERT 64			

RESULT 2
 US-09-470-946-6
 Sequence 6, A
 Patent No. 63
 GENERAL INFORMATION
 APPLICANT: Y
 APPLICANT: C
 APPLICANT: G
 APPLICANT: G
 APPLICANT: B
 APPLICANT: B
 TITLE OF INVENTION
 FILE REFERENCE
 CURRENT APPLICATION NUMBER
 CURRENT FILING DATE
 EARLIER APPLICATION NUMBER
 EARLIER FILING DATE
 NUMBER OF DRAWINGS
 SOFTWARE: PER
 SEQ ID NO 6
 LENGTH: 873
 TYPE: PRT
 ORGANISM: HU
 FEATURE: -
 OTHER INFORMATION
 US-09-470-946-6

RESULT 3
US-09-438-906-2
; Sequence 2, Application US/09438906
; Patent No. 6465155
; GENERAL INFORMATION:
; APPLICANT: Goldine, Ira
; APPLICANT: Trischitta, Vincenzo
; APPLICANT: Pizzuti, Antonio
; APPLICANT: Viglieri, Riccardo
; APPLICANT: Frittitta, Lucia
; TITLE OF INVENTION: Polymorphic Human PC-1 Sequences
; FILE REFERENCE: 9076-089
; CURRENT APPLICATION NUMBER: US/09/438, 906
; CURRENT FILING DATE: 1998-11-18
; PRIORITY NUMBER: 60/108, 853
; PRIOR FILING DATE: 1998-11-18

PRIOR FILING DATE: 1998-11-18

NUMBER OF SEQ ID NOS: 35
 SOFTWARE: FastSEQ For Windows Version 4.0
 SEQ ID NO 2 LENGTH: 873
 TYPE: PRT ORGANISM: H. sapiens US-09-438-906-2

Query Match 52.0% Score 2498.5; DB 4; Length 873;
 Best Local Similarity 53.1%; Pred. No. 8e-235;

Matches 465; Conservative 137; Mismatches 250; Gaps 11;

Qy 10 EQPVTRK----NTLK-- KYKACIVLALLVLMVSLGLGLGLRKEKGSPRKCFDAS 62
 Db 65 F---GNCRCDAACTVBLNCLDQETCCEPEHWTCKNSVCLTILGKPSCAKEVKSCKGRCFERT 64

Qy 123 KDCCADYKSVCOGETSWLEENCDAQQSCQPEGFDLPPVILFSMDGPRAEYLTTWDTLMP 182
 Db 122 GDCCINYYSSVCOGEKSWEWPCEINEQOCPAGEFTPTLFLDGFRAEYHTWGGLP 181

Qy 183 NINKLKTCTGTHSKYKMRAMYPTKTPRNHYTIVTGLYPHEHGIDDNMMYDVNLNKNESSLK 242
 Db 182 VISLKKKCGCTTYKMRPYPPTKTPRNHYTIVTGLYPHEHGIDDNMYDPKNASFSLSK 241

Qy 243 EQNPFAWQGPWLTAMYQGLKATYTFPGSEVAINGSFPSLIMPINGSVPFERISTL 302
 Db 242 EKENPENWYGEPIPAWTAKYQGLISGTFWPGSDEVEINGFPDPDLYKMYNGSVPFEERLAV 301

Qy 303 LKWLDLPKAERPRFYTMYFEEPDSSGHAGGPVSARVIRALQYVDHAFMLMELGKORNHL 362
 Db 302 LQWQLQPLPERPHFTYLKEEDPDSSGHSQGPVSEVIALQRDGMYCLMGLKELNHL 361

Qy 363 NCVNILLADHGMDOTYCNKMEYNTDYPRINFFYMEPGPAPRIRAHNPHDFFSENSE 422
 Db 362 RCLNLLIISHGGMQGSCCKRYIYUNKLQEDVKNIKVIGPAABLRPSDVKYTSNEYG 421

Qy 423 IVERNUSCRKEDDQHKPKYLPDLPLKBLHAKANVRIDKVLFEVDQW-LAVERSNTNGGG 481
 Db 422 IARNISCREPNQHFKPYLKHFLPLRPLHAKSDRLEPLTYLDQFWQLLNPSRKYCSG 481

Qy 482 NHGYNNEPRSMEAFLHAGPSPEKTEVAPPFENIEVNMCDLRIQDAPANGTHGSLAH 541
 Db 482 FHGSNDNPSPMDQALFVYGRGEFKICIAUTEVNMCDLNLTPAPNNTHGSNH 541

Qy 542 LLKVBFYEPFHAEVSKFSVCGFANPLPBLSDFC-PHQNSTQLEBVONQMINLTOEBI 600
 Db 542 LLKNPVTYTKHPKVEHPLQCPFTRN-PRDNLGSCSNESI--LPIEDFOTQFNLYTAAE 597

Qy 601 TATVYKVLPGFPRVYKTDQHCLLYHREYVSGFGKAMEMPMWSSYTVQLGPDTSPLPPT 660

Db 598 KLIKHTBLPGRPRVYKTCILQKENTICLISQHQMSGYSDHMLPLWTSYDTR--NDSFSTD 655

Qy 661 VPDCLRADYVPPSESOQCSFYLADKNTITHGFLYPPAASNRTSDQY-LEALITSNLVMYE 719
 Db 656 FSNCIYQDFRIPSLSPVHKCSFYQNTKVSTGFLSPQNLKNSGTYSEALLTNIVMQ 715

Qy 720 EFRKWDYFESVLLIKHATERNGYNVSGPIEDNYDGHFADPDEITH--LANTDVPBI 776
 Db 716 SFQVJWRYFHDTLKRYAERNGYNVVSGRVFDFDGRCDSLNLRQRRVVERNOELLI 775

Qy 777 PTHFFVVLTSKNSKSHTPENCPGMWDLPLPIPHRPTNYESCPGKPEALWVERFTAH 836
 Db 776 PTHFFVVLTSKNSKSHTOPPLHCEN-LDTLAFLPHRTDSECVHKGHDSSWBELLMLHR 834

Qy 837 ARVRDVELLTSKNSKSHTPENCPGMWDLPLPIPHRPTNYESCPGKPEALWVERFTAH 871
 Db 835 ARITDVEHITLSSYFQQRKEPVSDLKLTBLPTF 869

RESULT 4
 US-09-392-946-1
 ; Sequence 1, Application US/08392946
 ; Patent No. 5939269
 / GENERAL INFORMATION:
 / APPLICANT: Genentech, Inc.
 / APPLICANT: The Regents of the University of California
 / APPLICANT: Goldfine, Ira D.
 / APPLICANT: Gruppe, Andrew
 / APPLICANT: Maddux, Betty A.
 / APPLICANT: Stewart, Steven
 / APPLICANT: Timothy A.
 / TITLE OF INVENTION: Antagonists to Insulin Receptor Tyrosine
 / NUMBER OF SEQUENCES: 1
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 1 DNA Way
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Winpatin (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/392,946
 / FILING DATE:
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/182241
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Kubinec, Jeffrey S.
 / FILING DATE: 14-JAN-1994
 / REGISTRATION NUMBER: 36,575
 / REFERENCE/DOCKET NUMBER: P0875P1PCT
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 650/245-8228
 / TELEFAX: 650/952-9881
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 926 amino acids
 / TYPE: Amino Acid
 / TOPOLOGY: Linear
 / US-08-392-946-1

Query Match 52.0%; Score 2498.5; DB 2; Length 925;
 Best Local Similarity 53.1%; Pred. No. 8.e-235;
 Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;

Qy 10 EOPVKK---NTLK--KYKACIVLALLVIMSTGLGLGIGRLKLEQGSCRKCFDAS 62
 Db 57 EEPLEYAARARTAKDNTYKVLSSVCLTLLGCIFGKPSAKEVSKGRCFERT 116

Qy 63 FRGLENCRCDYACKORGDCCMDFEDTCVESTRMNKFQGETTEIASLSCSDCLK 122
 Db 117 F---GNCRCDAAVGLNCUDYQETCIEPHINTCNKFQGEKLTSLCSDCKD 173

Qy 123 KDCCADYKSVCOGETSWLEENCDAQOQSQCPEGFDLPPVILFSMDGFRAEYLYWDTLMP 182
 Db 174 GDCINNTSSVCGEKSVEEPQCPAGEFEPPTLISLDGFRAEYLHTNGGLP 233

Qy 183 NINKLXTCGIHSKYMRAAMYPTKTFPNHYTITGLYFESHGIDNNMYDYNLINKFPLSSK 242
 Db 234 VTSKLLXCGTGYTKNMRVYPTPTEPHYSTVGTGLYFESHGIDNNMYDYNLINKFPLSSK 243

Qy 243 EQNPFAWQHGPWMLTAMYQGLKATYTFPGSEVAINGSFPSLIMPINGSVPFERISTL 302
 Db 294 ERFNPENYKGEPIWVTAKYQGLKGTFWPGSDVDELVNGIFDIYQMGVSVPFBRILAV 353

Qy 303 LKWLDLPKAERPRFYTMYFEEPDSSGHAGGPVSARVIRALQYVDHAFMLMELGKORNHL 362

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/182241
 FILING DATE: 14-Jan-95
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0875P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/25-8228
 TELEX: 415/952-9881
 TELEFAX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 925 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-504-169-1

Query Match Score 2498.5; DB 2; Length 925;
 Best Local Similarity 53.1%; Pred. No. 8.8e-235;
 Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;

Qy 10 EQPVK---NTLK--KIRIACIVLALLIVINSLLGLGLGLRKLEKGSCRKCFDAS 62
 Db 57 EPEPLKAAPARTADPNPKVLSIVSIVCUTILGICFGKLRSCKAEVKSGRCERT 116
 Qy 63 FRGLENCRCDVACKDGDCCWDPEPDTCVESTRIMCNKFRCGETRLAASLCSDDCLQK 122
 Db 117 F---GNCRCDAACTELGNOLDQETCBEPEHWTNCFRGKEKLRTSLCACSDDKDK 173
 Qy 123 KDCCADYKSYCVOQGTSLWENCITAQQSOCPEGFDJPPVILPSMDGFAEYLTYDQJMP 182
 Db 174 GDCCINYYSSVCQGBBSWVEBPCBSEINPQCPAFETPTLFLDGRAEYHTWGDLLP 233
 Qy 183 NINKLTCTGITHSKYMRAMYPTKTRFPNHYTTIGLYPESHGIDANMMVDNKNFSSSK 242
 Db 234 VISTKLKCGTNYQNPYPTKTFPNNHYSIVTGLYPERHGIDDNKMDPKRNASFSLSK 293
 Qy 243 BONNPWWHGQPMWLTAMYQGLKAATYFWPGSEVAINSSFPSTYMPNGSVPFERSTL 302
 Db 294 EKFENPEWYKGEPIWVTARYQGLKSGTFFWPGSDVEINGIFPDYKMYNGSVFEERLAV 353
 Qy 303 LKWLDLPRDERPHFTYTLLEPPISSGSYGPISSEVFKALQVTDHAFGMLMEGLKQRNLH 362
 Db 354 LOWIQLPDRDERPHFTYTLLEPPISSGSYGPISSEVFKALQVTDHAFGMLMEGLKQRNLH 413
 Qy 363 NCVNILLIADHGMDQTYCNKMEYNTDYEPRIIRAHNIIPHDFFSNSEE 422
 Db 414 RCUNLNLISDHGMEQGSCKKKVYLNKQLGDVNKIVYQPAELRPSVPDKYKSYFNEYG 473
 Qy 423 IVRNLSCKRPDKDQFKPLTPDLPKRHLHYAKNVRIDKTHLYDQW-LAVRSKSNTNCGG 481
 Db 474 IARLJSCEPNQHFRPyJRHFLRFLFAKSRIEPTFLYDLPQWQALNPBKRYCGSG 533
 Qy 482 NHGYNNEPESMEAIFIAGHPSEPEKTEVPEPENNIEVNLMCDLRLQCAPNGTHSINH 541
 Db 534 FHGSDDNIVSNMQALFYGPGPFGHGIADTFTENIETVNLCDLNNTPAPNGTHSINH 593
 RESULT 5
 US-08-504-169-1
 Sequence 1, Application US/08504169
 ; Entity No. 5968508
 ; GENERAL INFORMATION
 ; APPLICANT: Goldfine, Ira
 ; APPLICANT: Grupe, Andrew
 ; APPLICANT: Henzel, William
 ; APPLICANT: Maddox, Betty
 ; APPLICANT: Spener, Steven
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Harrison, Denise M.
 ; TITLE OF INVENTION: Antibodies to Insulin Receptor Tyrosine Kinase Activation Inhi
 ; NUMBER OF SEQUENCES: 1
 ; COMPUTER READABLE FORM:
 ; ADDRESSSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; MEDIUM TYPE: 5.5 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/504,169
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/14893
 ; FILING DATE: 28-Dec-1994
 ;
 ; 708 FSQVLYQDFRIPLSPVHKCSFVKNNTVSIQGLSPPLNNSGIVSEALITNI/PMQ 767
 ; 720 EFRKMWYDFHSVLLIKHATERGVNVYSGPFDNYDGHFADPDEYTKH--LANTDVP1 776
 ; 768 SFQVLYWYFHDTLLRKTAEBERGVNVYSGPFDYDGRCDSLENLNRQRRRVIRNOELI 827

Qy 777 PTHYFVYLTSCKNSKHTPENCPGNLDVLPLPIIPIHPTNVESCPSEGKPBALMVEERTAHI 836
 Db 828 PTHFFPLSKDTSQTPLHCEN-LDTTAAFLHRTDSECVHGRHDSSEVELMLHR 886

Qy 837 ARVDYVEELLTGDFYQDKYQPVSEILLQIKTYLPTP 871
 Db 887 ARITDVEHITGLSFYQRKEPVSDILKTKLTHLPTF 921

RESULT 6
 PCT-US94-14893-1
 / Sequence 1, Application PC/TUS9414893
 / GENERAL INFORMATION:
 / APPLICANT: Genentech, Inc.
 / APPLICANT: The Regents of the University of California
 / Goldfine, Ira D.
 / Grube, Andrew
 / Maddux, Betty A.
 / APPLICANT: Spencer, Steven
 / APPLICANT: Stewart, Timothy A.
 / TITLE OF INVENTION: Antagonists to Insulin Receptor Tyrosine Kinase Inhibitor
 / NUMBER OF SEQUENCES: 1
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 460 Point San Bruno Blvd
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Pacin (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: PCT/TUS94/14893
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/182241
 / FILING DATE: 14 JAN 1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Kubinec, Jeffrey S.
 / REGISTRATION NUMBER: 36 , 575
 / REFERENCE/DOCKET NUMBER: 875P1PCT
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415/952-9881
 / FAX: 910/371-7168
 / INFORM. FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 925 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / PCT-US94-14893-1

Query Match 52.0%; Score 2498.5; DB 5; Length 925;
 Best Local Similarity 53.1%; Pred No. 8.8e-235; Mismatches 250; Indels 23; Gaps 11;

Matches 465; Conservative 137; Sequence ID NO: 1:
 57 EEPLEKAARARATAKDNTYKVLSSVCLLTIGCFGLKPSCAEVKSCKRCFERT 116

Qy 63 FRGLENCRCDVACKORGDCWDFEDTCVBSTRIMCNKPRCGTRLEASLCSCDCIQLK 122
 Db 117 F--GHRCRDIAACVNLGNCCLDYQTCIEPEHHTCNKPRCGTRLEASLCSCDCIQLK 122
 / SEQ ID NO 4
 / LENGTH: 873
 / PRIORITY: 1998-11-16
 / NUMBER OF SEQ ID NOS: 35
 / FILE REFERENCE: 9076-089
 / CURRENT APPLICATION NUMBER: US-09-438,906
 / CURRENT FILING DATE: 1999-11-18
 / PATENT NO. 6465185
 / GENERAL INFORMATION:
 / APPLICANT: Goldfine, Ira
 / APPLICANT: Trischitta, Vincenzo
 / APPLICANT: Pizzati, Antonio
 / APPLICANT: Vigneri, Riccardo
 / APPLICANT: Frittitta, Lucia
 / TITLE OF INVENTION: Polymorphic Human PC-1 Sequences

Qy 10 EQPVKK----NTLK---KYKIACTIVLLALIVIVMSLGLGLGLRKLEKGSKRKCFDAS 62
 Db 57 EEPLEKAARARATAKDNTYKVLSSVCLLTIGCFGLKPSCAEVKSCKRCFERT 116

Qy 63 FRGLENCRCDVACKORGDCWDFEDTCVBSTRIMCNKPRCGTRLEASLCSCDCIQLK 122
 Db 117 F--GHRCRDIAACVNLGNCCLDYQTCIEPEHHTCNKPRCGTRLEASLCSCDCIQLK 122
 / SEQ ID NO 4
 / LENGTH: 873
 / PRIORITY: 1998-11-16
 / NUMBER OF SEQ ID NOS: 35
 / FILE REFERENCE: 9076-089
 / CURRENT APPLICATION NUMBER: US-09-438,906
 / CURRENT FILING DATE: 1999-11-18
 / PATENT NO. 6465185
 / GENERAL INFORMATION:
 / APPLICANT: Goldfine, Ira
 / APPLICANT: Trischitta, Vincenzo
 / APPLICANT: Pizzati, Antonio
 / APPLICANT: Vigneri, Riccardo
 / APPLICANT: Frittitta, Lucia
 / TITLE OF INVENTION: Polymorphic Human PC-1 Sequences

Qy 123 KDCCADYKSVQGETSMLENCDTAQSQCPEGFDLPPVILFSMDGFAEMLYTWTDLMP 182
 Db 174 GDCCINNSVSVQGEKSWEEPECS-NEPOCPAGETPTPTLPSLDGFAEYLHTWGGLLP 233

Query Match 51.9%; Score 2494.5; DB 4; Length 873;
 Best Local Similarity 53.0%; Pred. No. 2e-234;
 Matches 464; Conservative 138; Gaps 11;

Qy 10 EQPVK---NTELK---KYKIACTYLLATLIVINSLGLIGLIRKLEQSGCRKCFDAS 62
 Db 5 BEPLEXAARTARDPNTYKLSVLTLGICFLPKSCAEVKSGRERFER 64

Qy 63 PRGLENCRDVACKDRGDCWDFDTCYBSTRIMCNKRCGETRLASLCSDDCLOQ 122
 Db 65 F--GRNRCDAACYVELGNCCOLDYCETCTPEH-WTCNKRCGEKLRTRSLACSDCKDQ 121

Qy 123 KDCCADYKSYCQGETSWLLENCTAQQSOSCPEGFDLPVILISMDGPRABLYTWTDLMP 182
 Db 122 GDCCCTNYSYSCQGERSWEPCESSINEPQCAPSAPETPTLIELDGFRAYLTHTNGLLP 181

Qy 183 NINKLKTCGHSKSYNRAAMPPTKTPNHYTIVTYPESHHGIDDNMYDVNLNNRPLSSK 242
 Db 182 VLSLKKCGCTYTKNMKRPVYPTKTPNHYTIVTYPESHHGILDNKMDPKRNNAFELSK 241

Qy 243 EQNNDPAWHQPMWLTAMYKGLRATYTFPGSEAVINGSFSTIMPYNGSPFEERISTL 302
 Db 242 EKENPEWKGEPIWTTAKCGLEKGSTFPWPGSDEVINGIFPDYKMYNSVPEERILAV 301

Qy 303 RLWLDIPKAERPRFTYMFPEPDSSHAGGPVSEARVITALQVDHDAGMMLMEGLKORNHL 362
 Db 302 IQWLQLQPKEDERPHFYTLYLEPDSSGHSGVPSSEVIALQRVDGMVGMMLDGLKELNLH 361

Qy 363 NCVNIIILLAHGDMDOTYCNKRMEMNTDYPFRINPFYMEGAPRIRAHNIPDFFSENSEE 422
 Db 362 RCLNLILISDGMEGOSCKYYIINKYLGDRNTRKTVYGPARKLRSVDPIKYTSNEYG 421

Qy 423 IVRNLSCKRDQHERRPFLDPLPKRLHYAKNVRDVKYLFDQOW-LAVRQKSNTNCGGG 481
 Db 422 TARNLUSCREPNQHFKPLGHFLPKRLHAFARSDRLEPLTFLPQWQALNPSERKYGSG 481

Qy 482 NHGYNNEFRSMEAATLAHGSPEKETKEVEPENIEYLNMCULRIOPAPNGTGSSINE 541
 Db 482 PHGSDIVFSNNQALVGYGGFKHGTEAFTFENIEEVNLMDLNUTPAPNGTHGSLSNH 541

Qy 542 LLIKVPYEPSEHAEVSKEFSCVGCFANPLPTESDLFCF- PHLNQNSTOLEQVNQMLNTOBEI 600
 Db 542 LIKNPVPTYRPHKPVPHLYQCPFPTRN- PRDNLGSCNFPI --LPTEDFTQFOFNUTVAE 597

Qy 601 TATVRYNLPGCRPRVYQDPLSPVYKSYKONTKVSYGFSLQKSYLADNITHGFLYPPASNRTSDSQY-DALITSNLYPMYE 719
 Db 656 FSQNLQYDQDFRIPPLSPVYKCSFYKONTKVSYGFSLQKSYLADNITHGFLYPPASNRTSDSQY-DALITSNLYPMYE 715

Qy 720 BFRKWDYFISVLIKHATAERNGVNVSGPFLDYNQHGFDADELTKH--LANDDVTPL 776
 Db 598 KIKKETLTYGRPRVLTQXENTICLILSOHFMSSYSDQDILMLPLNTSYTVDR- NDSEFSTD 655

Qy 661 VPDCURADRVYPPSESQKCSFYLADNITHGFLYPPASNRTSDSQY-DALITSNLYPMYE 719
 Db 716 SFGQVWRYFHDTLRLKYAERNGVNVSGPVEFDYGRCSLLENLRQKREVIRNQEILL 775

Qy 777 PTHYFWVLTCSKNTSHPTPNCPGWLFVIFLPHRPTVNECPEGKPEALVEERFTAH 836
 Db 776 PTHFFFVLTCSKDTISOTPLHCE-NLTIAFILPHRTDNECSCVHGRDHSSWEELMLHR 834

Qy 837 ARVDDVELLGLDQYQPVSEHILQKTYLDPFT 871
 Db 835 ARIDVEHHTGLSFIQQRKEPVSDILKUKTHLPTF 869

RESULT 8
 US 08-346-455B 69
 Sequence 69, Application US/08346455B
 ; Patient No. 5731167
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA, DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING

TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS: 69
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/346,455B
 ; FILING DATE: 28-NOV-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06613
 ; FILING DATE: 24-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 ; REGISTRATION NUMBER: 36,434
 ; REFERENCE DOCKET NUMBER: 2026-4149PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 751-6800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 69:
 ; SEQUENCE CHARACTERISTICS:
 LENGTH: 915
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: No
 FEATURE:
 NAME/KEY: A2058 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 US-08-346-455B-69

Query Match 42.5%; Score 2040.5; DB 1; Length 915;
 Best Local Similarity 40.5%; Pred. No. 5.2e-190;
 Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps 11;

Qy 24 ACTVLLAVIMSIGLGLGLRKLEK-----
 Db 9 SCQIISLFTFAGVSIOLGFTAHKRAEGMEEGPTVLSDSPTNISSSCKRCFELQE 63
 Qy 598 KIKKETLTYGRPRVLTQXENTICLILSOHFMSSYSDQDILMLPLNTSYTVDR- NDSEFSTD 655

Db 124 DCADIKSYCQGETSKLEENCDTAQSQCPBEGFDLPPVILESDGPRAEYLTYWDTLMPN 183
 Db 129 DCCTNRYCVCGRGESEHVVDDCEEIAECAECPAGEYRPLIFSVGDSFRASYMGKGSKTPN 188

Qy 184 INKLKTOGIHSKYMAMYPKTFPNHYTIVTGLYPSHGIIDNNMNDLNKNFSLSSKE 243
 Db 189 IEKLRSGTHSPYMRVYPTKTFPNUYLTATGLYPSHGLVGNMSYDPVFDATFLRLRRE 248

Qy 244 QNNPAWHAQPMWLTAMYQGLKAATYFWPGESEAVINGSFPSINPYNNSVPFEPRLSL 303
 Db 249 KENHRWKGQPLWITATKQGVKAGTFWW-----SVVIPH-----ERRILTL 290

```

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/345,455
FILING DATE: 28-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: No
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-69

Query Match Score 2040; DB 3; Length 915;
Best Local Similarity 40.5%; Pred. No. 5.2e-190;
Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps 11;

Qy 24 ACIVALLVITMSLIGLIGLGLRKLEK-----QSSCRKKCPDASF 63
Db 9 SQQIISLFTFAVGVSCLGFTFAHRKRAESWEEGGPPTVLSDSPATNISGCKGRCFELQE 68
Qy 64 RGLENRCDVACKDRGCDMDFEDTCVESTIWMCNKFRGEETRLEASLCSDDCLQKK 123
Db 69 AGPPDRCDNLICKSYTSCCSDFDELCLKTARGWEETKDRGEVNEENACHCSEDCDLARG 128
Qy 124 DCCADTKSVCGCGETSWLLEENDTAQSQOCQEGFDLPPVILFSMCGFRAYLYTDWTMLMN 183
Db 129 DCCTNTQVCKGEHSWVDDCEEIKAAECDAFGVRPLLIFSDVGEFRASYMKKGSKVMEN 188
Qy 184 INKLKTCGTHSKYMAFPKTFPKHYYTITGLYPSHKGQTIDNNMYDVNLNKNFSSLSSKE 243
Db 189 TEKRLRGCGTSPYMDVEVPTKTFPLIYTATGLPESRGIVGNSYDPFDATHLRGRG 248
Qy 244 QNNPAWKHGQPMWLTAMYQSKAATYFWPSSEVAINGSPSISYMPYNGSPVPEERISSL 303
Db 249 KFNHRWQGQWLWITATQKVAGFEFW-----SVIPH-----ERRLIT 290
Qy 304 KFLDILKAERBRPFYIMYFPEPDSSCHAGGIVSA-----336
Db 291 RWLTLDPHERPSVAYFSEQPDFSCKYGFPEESSYGSPTPAKRPKRQBR 350
Qy 337 -----RVIKALQVQDHAFGMLMEGLKORNHLNCUNILL 371
Db 351 EVAPPKERRQKTHRMHDHYAAETRQKMTNPLREDKIVGQLMQDGKQKLKRCYVIVFY 410
Qy 372 DHGMDOCTCNKMEYMDYEPRIINFMVYEPAPTR--AHNIPHDFFSNSEETVIRNL 428
Db 411 DEGMEDVTCRTEFLSNLVDDITLVPSTLGRRSKPSNNAKYD----PKAIANLT 465
Qy 429 CRKPDKDHEKPKYLTPDLPKRLHYAKNVRIDKVLFYDQW-----LAVRSKSNTNC-GGG 481
Db 466 CKKPDQHFKPKYLQKHPKRLHYANTRIEDJHLVVERVHARKPLDLYKKPSGKCPFQG 525
Qy 482 NEGYNNEFRSMEAIFIAGPSFSKEKTEVFENIEVYNLMCDLLR1QAPNNGTHGSNLN 541

```

RESULT 10
US-09-483-831B-69
Sequence 69, Application US/09483831B
Patent No. 6,173,338
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY
APPLICANT: LIOTTA, LANCE
APPLICANT: SCHIFFMANN, ELLIOTT
APPLICANT: KRUTZCH, HENRY
APPLICANT: MURATA, JUN
TITLE OF INVENTION: AUTOTOXIN: MOTILITY STIMULATING PROTEIN USEFUL IN TREATMENT OF INVENTION: CANCER DIAGNOSIS AND THERAPY
FILE REFERENCE: 2026-4149054
CURRENT APPLICATION NUMBER: US/09/483, 831B
CURRENT FILING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 07/892, 043
PRIOR FILING DATE: 1992-01-17
PRIOR APPLICATION NUMBER: 08/249, 182
PRIOR FILING DATE: 1994-05-25
PRIOR APPLICATION NUMBER: 08/346, 455
PRIOR FILING DATE: 1994-11-28
PRIOR APPLICATION NUMBER: 08/977, 221
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 69
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Polypeptide
US-09-483-831B-69

Query Match Score 2040.5; DB 4; Length 915;
Best Local Similarity 42.5%; Pred. No. 5.2e-190;
Matches 379; Conservative 177; Mismatches 268; Gaps 11;

Qy 24 ACIVLIALTMSLGIGLRLDEK-----QGSCRKKCEDASP 63
Db 9 SCQIISLPLFPAVGVISICLGFATARIKRAEGWEGPPTVLSDSPWTNISGCKGRCFELQK 68
Db 64 RGLENCRDVAACKDORGCCWDFFCVERSTRNCNKFTRASLSSDDCLOK 123
Qy 69 AGPPDCRCNDLCKSYTSCHEDDLCLKTARGMECTKDRGCEVRNEAACHSEDCLARG 128

Qy 124 DCCADYKSVQCGETSWIBENCDTAQOSQCPEGFDLPPVILESMDDGFRAEVLYMTDLMPN 183
Db 129 DCCTNYQVYCKGESEHWTDDCEBEIAAECAGFVRPLIFFSVDGFRAASYMKGSKVME 188
Qy 184 INLKTCIITHSKYMRANTPKTFPNEYHTVITGLYSESGTIDNNYDVNLANKPSLSSKG 243
Db 189 TEKIRSGTHSPMRYPPKTFPMLYLTATGLYFBSHGVGNSMYDPVYDAPFLRGRB 248
Qy 244 QNNPAWEGQPNMLTANYGKAATYFWPGSEVAINGSPFSIYMEYNGSVPFEERISTTL 303
Db 249 KFNHRWMCQPLWITAKQGYKAGTPW-----SVVIPH-----EBRILITL 290
Qy 304 KWLDLPAERPRPYTMFEEDPSGHSAGGPVSA----- 336
Db 291 RWLTLPDHERPSVYAFYSEQPDSFGHKYGPGPBESSYGSPPFTAKPKRKVAPKRQRER 350
Qy 337 -----RVTKAHQVWDBAFCNLIMEGIKQRNLHNCHCNNTILLIA 371
Db 351 PVAPPKGRRRKTHRMHDYAAETRQDKTNPREIKVGJLMDGAKQLKLRCRNVIYFG 410
Qy 372 DHMDQTYCNCNKEYMTDFPRINFFYMEGSPAPR-----AHNTPHDFFSFNSSEBIVRNLS 428
Db 411 DRHMDTCDRTEFLSMLTNDTIVDPLVPGTLGRTRSKFNSNAYD-----PRAJALND 465
Qy 429 CRKPDPDKPKPVLTPDPLKRLHYAKNVRDVKHFLVDQON-----LAURSKSNTNC-GGG 481
Db 466 CRKPDPDKPKPVLTKHFLVARKPLDVKRPSKCFRQG 525
Qy 482 NQYNNPERSMMAELHLGSPFKETEVPEENIYNNMCDLRLQAPANGTHGSLNH 541
Db 526 DHSFDNCKVNSMOTVFGYGPFTKVKPFENTLYNCNCDLGLKPAPNNGTHGSLNH 585
Qy 542 LLKUPFTEPSHAEEVSFKPSVCGFANPLPTSLDCEC-PHQLNSTOLQBLQVNQMLNLTQBEI 600
Db 586 LIRTNTTRPTMEEVTRPNYGINMQLQSDDELGCTCDPKNLDELNKRHTK---- 641
Qy 601 TATVKVNLPGPRLVQVNDHCLLYREVSGFGKAMRMPMWSSTYVQLGDTSPPLPPT 660
Db 642 GSDEERHILYGPAPYLX-TRYDLYHTDFESGYSEIELMLLWSYTYSKQAEVSYDH 700
Qy 661 VPDLRADMVRVPSSESQKCSYTLADKNTHGFLYPPASRNTSDSQYDALITSNIVPMYEE 720
Db 701 L1SCVRDPDVRSPSFSONCLAYKNDKQMSIGLFFPPLSSSPEAKYDAFLVTMVPMYPA 760
Qy 721 FRKWDYFPHSVLILKHATERGVNVVSGPFDYNTDGHFADPDEIKLHANTDVFPIPHY 780
Db 761 FKVWNFTQRLVVKCAYSERGVNVVSGPFDYDGLHDTEDIKQTYEGSSIPVPHY 820
Qy 781 FVVLTDKSNKSHTPENCPGWLDVLPPTIPIHPRPTNVECPGKPPRALWEERFTAIIARVR 840
Db 821 YSITSCUDFTOPADCDGPUSVSSFLPRPDNECSNSSEDESKWVEELMKHNTARVR 880
Qy 841 DVELITSLDFPRTKTSRSTSYPLTLYTLYSEI 875
Db 881 DIEHLTSLSDFPRTKTSRSTSYPLTLYTLYSEI 915

RESULT 11
PCT-US95-06613-69
Sequence 69, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LICHTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGIAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK

COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE DOCKET NUMBER: 2026-4149US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 751-4400
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 915
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: No
 FEATURE:
 NAME/KEY: A2058 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PCT-US95/06613-69

Query Match 42.5%; Score 2040.5%; DB 5; Length 915;
 Best Local Similarity 40.5%; Pred. No. 5.2e-190;
 Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps 11;

QY 24 ACIVLLAVLVLIGLGLIGLGLRKLK-----QQSCRKCFDSF 63
 Db 9 SCQISLFTFAGVSGICGFTAHRIAGWEGPPTVLSDPWTNISSSCKRCFQE 68

QY 64 RGLENCDCVACKDGGCCWDPEDTCVESTRIWMCNKFRGETRLEASLCSCSDCLKR 123
 Db 69 AGPPDCREDNLCKSYTSCHDDELCKTAGWECKDRGEVNBENACHCSBDSLARG 128

Qy 124 DCCADYRSVCQGERTSWLEENCDAQQQCPSGFDLPVILFSMDGFRAEYLWDTIIPN 183
 Db 129 DCCTNYQVCKGBSHWYDDCEIKAECPAGEVRPLIFSVDGFRASYMKGSKYNP 188

Qy 184 QNNPAWHQPMWLTAMYQGLKATATWPGSEVAINGSFPIIMPYNGSVPFEERISTIL 303
 Db 249 KFNFRWGGQPLWATAKGQVAGTFTW-----SVVPH-----ERRIL 290

Qy 304 KMIDLPKAEPRPYTMFEEPDSSGAGGPVSA-----336-----
 Db 291 RWLTPDHERPSYAFZSBQDPSGHYGPPEESSGSFTPAKRKVAPKRRBR 350

Qy 337 -----RVIKALQVUDHAFGMLMEGLKORNHLNCYNTILLIA 371
 Db 351 PVAPPKERRRKTHRMDHYAETRQDKTNPREIDXVGQLMDGLQLKLRCYNTIVFG 410

Qy 372 DHGMOTYCNRMBYMTDYPRINFFYMEGAPRIR--AINTPHDFSFNSEETIVRNLS 428
 Db 411 DHGMEDVTCDRTESLNLYTNVDITLVPGTLGRRSKPSNNAKYD---PKAIANLT 465

Qy 429 CRKPQHFKYLTPLRKYLHARNVRDKVHIFVDOOW----LAVERSNTNC-C-GGG 481
 Db 466 CKKPQHFKYLQHOLRKLRYHANNRVEDHILVERWHARKPLDVYKKPSCKFFQG 525

Qy 482 NHGYNEFRSMEAIALFRLQPSFKETEVEPFENIETYVNLMCDLRLIQAPNGTHGSLLNH 541
 Db 526 DHGFNKRVMQTYFVGQPTFKTKPFPENIELINVMDCLLGZPAPNGTHGSLLNH 585

Qy 542 LLKVDPYEPHAEVSKFESVCGFANPLTESLDCFCLPHONSTOLEVQNMNLQEEI 600
 Db 586 LLRTRNFRPMPMEETRPNPGMILQSDDFLQCTDDKVEPKNKDLDELNKLHTK--- 641

Qy 601 TATVYKNLPEGRPRVLUQKNDVHCLUYHEYYVSGFGKAMRMPKWSSTYPOGLDTSP1.PPT 660
 Db 642 GSTERBLHLYGRPAVLRY-TRYDLYHDFESESYEFLMLWTSVSKQEVSSVPDFH 700

Qy 661 VPDCRADYEVPPSESOKSFEYLAQDNITHGELYPASNRTSDSOYDALITSNLVPMYEE 720
 Db 701 LrscrPdVrVsPSSQNLAYKDQNSYGFELPPTLSSPAAKYDAFLVNMPYPA 760

Qy 721 FKRMDFPHSVLILKHATBRGNGNVUSGPIEDYDNGDHFADDEITKHLANTDVPPTHY 780
 Db 761 FKRVNMYFORVLYKXASERGNVVISCPFDYDGHDTEDKIQYVEGSSIPVTHY 820

Qy 781 FVVLDSCKNSKSHTPENCPWMLDVLPIFIPHPRNVESEPGPEALWYTERSTAHTARV 840
 Db 821 YSIIISCLDTQPAKCDQPLSYSSFLPHRPDNEESNSSEDSEKVAEELMKMHTARV 880

Qy 841 DVELLTGLDFYQDVKQPVSRILQKLYPTFETI 875
 Db 881 DIEHTSLSDFERKTSRSYFEILTKLYHTYESEI 915

RESULT 12
 US-08-346-455B-34
 ; Sequence 34, Application US/08346455B
 ; Patent No. 5731167
 GENERAL INFORMATION:
 APPLICANT: UNITED STATES OF AMERICA; DEPT.
 APPLICANT: OF HEALTH AND HUMAN SERVICES
 TITLE OF INVENTION: MOILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 NUMBER OF INVENTION: THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994
 CLASSIFICATION: 520
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043

FILING DATE: 17-JAN-1992
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36, 434
 REFERENCE DOCKET NUMBER: 2126-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-8800
 FAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 829
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: Protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: Putative protein
 US-10-005-456-B-34
 OTHER INFORMATION: sequence of A2058 Autotaxin
 Matches 363; Conservative 164;
 Score 1964.5; Pred. No. 1,2e-182; Length 829;
 Best Local Similarity 42.4%; Mismatches 239; Indels 91; Gaps 10;
 Query Match 40.9%; Score 1964.5; Pred. No. 1,2e-182; Length 829;
 Matches 82; CWDDEDTCVSTRIMCNKFRGEGTRLEASILCSDDCQKKDCCADYKSVCGGETSMWLE 141
 Db 1 CHDDDELKTAARGWBETDRGEGVRNEAHCSEDCLARGDCCTNQQVCKGEHWID 60
 Qy 142 ENCDTAQSSCOPPEGFLPPLVFSMDGFRELYTWDTIMPNNKLTKGIGISKNMAY 201
 Db 61 DDCBEIRKAATCAGFTRPPLIFSTDFGRASYMKRGSKMPTEKLQRGKPSYKPY 120
 Qy 202 PRKTFEPHYTIVTGlyPSEGHLIDNMYDVLNKNFNSLSKSEQNPNPAWNGQPMWLAMY 261
 Db 121 PTKTFPNLYTATGlyPESHIGVGNMIDVFDATFHIGREKFHNHMGGLPLWITAK 180
 Qy 262 QGLKAATYFWPGCEVAINGSPSITMPNGSVPPFEERISSLKWDLPKAEPFRFTMF 321
 Db 181 QEVKAGTCFV-----SVVIPH-----ERRITLRLWLTLPDHERESVAFYS 222
 Qy 322 EPPDSSHAGGPUSA ----- 336
 Db 223 EQPDFSSHKYSPGPBESSYGSPTFPAKEPKRKRQERPVAPPKKRRKIKHMHDY 282
 Qy 337 -----RVITALQVVDHAFGMLAEGLKGORNHLNCVNNTILLAHGMDOTYCNRMETMYD 389
 Db 283 AAETRDQKMTNPRLREDKTIVQLDQLKQLKLRQCVNIVFVGHGMEDVTCDRTFELSY 342
 Db 390 FPRINFYYMVEPAPRIR --AHNPDPFFSFNSBEIVRNLSCKPDQHFRYLTPDLPK 446
 Db 343 LTNVDDITLVPGTLGRISRFKESNNAKYD---PKAIANLITKPKDHPKPYLQHLPK 397
 Qy 447 RLHYAKNRVIRIDKVHLFVDDQW----LAVRSKSNNTNC GGGNHGTYNNEFRMEALFLAH 499
 Db 398 RLHYANRRIEVDIHLIVERMWHVARKPLDYKXPSGKCFQGDHGFDKVNMSMQTVFGY 457
 Qy 500 GPSFKERKTEVEPFENIEVNLCDLRLRIOPAPNGTHGSNLHLLKVPYEEPSHAEEVSK 559
 Db 458 GPTFKXKTRVPPFENIELAVNCDLGLKEPAPNGTHSSLNHLRTRTFRPMPPEEVTRP 517

Qy 560 SVCGFANPLPTESDLDCFC - PHLONSTICOLEQVNQMLNLTQEETIATVKNLDFGRPRVLQK 618
 Db 518 NYPGTMYLQSDDDDGCTDDKVKPKNKDELMKRLHTK---GSTERHLLYGRPAVLYR 573
 Qy 619 NVDHCLHYREYVSFGKAMRMVBMWSYTVPOLGDTSPLPPTVDPDCIRADVTRVPSSESQK 678
 Db 574 -TRYDILHHTDPESGYSEFMLMWTSYTSKQAEVSUPDHLSCTRDPDRVSPFSQN 632
 Qy 679 CSFYLAQDNITHGGLYPPASNRNTSDOYRDLATTSNVPYMEPEFRKMDYFHSVLLIKHAT 738.
 Db 633 CLAYNDKDNKSYGFLPPYLSSPEAKDAAFLVNMVPMYPAFKRWNYQFRLVRYAS 692
 Qy 739 ERGNGVNVSGPIFFYDGHFDADDETKHLANTDVIPTHYEWVLTSCFNKSHTPENCP 798
 Db 693 ERGNGVVISCPIDFYDGLHDTEDKQYBGSSTIVPHTYSSITISCLDFTOPADKCD 752
 Qy 799 GWLDVLPFLPHPTNVNSCPCGKPEALWEEFRTAHARVDRDVELLGDFYQDXVQPV 858
 Db 753 GPLSVSYSPFLPHRDNECSNSSEDESKWVEBLMKQETARVDRDIEHLLSDFRKTSRSY 812
 Qy 859 SEILOJKIYLPFTETTI 875
 Db 813 PEILTKTLYLHTYESETI 829

RESULT 13
 US-00-977-221-34
 / Sequence 34, Application US/08977221
 ;
 ; Patent No. 6,084,669
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA: DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TREATMENT
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/977, 221
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/346, 455
 ; FILING DATE: 28-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249, 182
 ; FILING DATE: 25-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/922, 043
 ; FILING DATE: 17-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DOROTHY R. AUTH
 ; REGISTRATION NUMBER: 36,434
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4000
 ; TELEX/FAX: (212) 751-849
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 829
 ; TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: Protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD: Putative protein
 OTHER INFORMATION: Sequence of A2058 Autotoxin

1-08-977-221-34.

Query Match Score 1964.5; DB 3; Length 829;
 Best Local Similarity 42.4%; Pred. No. 1.2e-182;
 Matches 363; Conservative 164; N mismatches 239; Indels 91; Gaps 10;

82 CWDFFDTCESTRWMCKNCRKCGTRELASLCSDDCLQKDKCDAKDYKSCVQGETSWL 141
 1 CHDFDELCKTARGWCTKDRGTYNEAACHSEDCLRGDCCTNYQVICKGBSHWVD 60

142 ENCDTAQOSOCOPREGFLPPLVIFSMGDGFREAYLTWDTLMPNINKLKTCGTHSKYRAMY 201
 61 DICEEKAACEPAGFPRPLIIFSVDGFRASYMKGSKMNPTEKLSCGTISPYRPVY 120

202 PTKTFPWNHYTIVTGlyPESHGIIIDNNMYDYNLNKNFSSLSSKEONNPawHGGOpMwLTAMY 261
 121 PTKTFPWNLYTATGlyPESHGIVGNSMDPFDATFHGREKENHRAWGGQLWLWATK 180

262 QGLKAKATYFWPGSEVIAINGSFPSPSYIMPYNGSVPFEERISTLKLWLDLPAKAERPRFYMF 321
 181 QSVKAGTFWV-----SVYPH-----ERRITLIRWLTLFDHERPSVAFYS 222

322 EPPDSCHAGGPVSA-----336

223 EQPDPSCHAGKYGFGPDESSYGSPPFTPKRKRKVKAPKRKRQERPVAPPKRKRKHRYDHY 282

337 -----RVTIALQVVDHAFRMNLMEGLKORNLENCAVNILLAHGMDDTYCNKNEYTDY 389
 283 AAETQRDKMTNPLRETDKIVGQLMGKLQKLRCCVNY_FVGDHGMEDYTCTRFELFSNY 342

390 PFRINFFYMEBPAPlR--AHHN_PHDFFSFNSEEIVNLNSCRKPDKHFKPLTPLPK 446
 343 LTNVDDTILVETGTLGRSKRSKESNNAYKD----KATIANLTCKKPDQHKYKLQHLPK 397

447 RLHYAKNVRIDKVLHVFDQW----LAVRSKSNTNC_GGGHGYNEFRSMEAFLAH 499
 398 RUYHANRRIEDHLLVERRHVARKPLDYKPGKCPFOGDHGFDNKVNMSMQTVFGY 457

500 GPSFKETEVPEPFENIEVYNUMLCDLRLIOPAPNNGTGSLNHLKVPFYEPHAEYSKF 559
 458 GPTEKYKIKVPPFENTELYNMCDLIGLKPAPNNGTGSLNHLRTINTFRPTIMEETVRP 517

560 SVEGRANFLPFTBSLDFC_PHQNSTOLEQYNOMLNQEETIAVKNLPEQRPRVYQK 618
 518 NYGMYLWQSDDLGCTCDKVEPKRNKLHTK---GSTEEHHLIGRPATYL 573

619 NVDHCLLHYREYVSGFQKAMMMPMSYYTVPQGDTSPLPPTPDCLRADVYPPSSQK 678
 574 -TRYDILYHTDESGSEIFMLLWNSYTSKQEEVSSYDPHITSVRDPVSPSSQN 632

679 CSYLAQKNNITGFLYPPASNRTSDQYDALTUNLWPMYEFKMMWDFHSTLLIHFAT 738
 633 CLAYKNDKOMSYGFLPFLPFLSSPEAKYDDEFLVNMVCPYTPAFAVNVYFORTLVCKAS 692

RESULT 14
 US-09-483-831B-34
 ; Sequence 34, Application US/09483831B
 ; Patent No. 641338
 ; GENERAL INFORMATION:
 ; APPLICANT: STRACKE, MARY
 ; APPLICANT: LICOTTA, LANCE
 ; APPLICANT: SCHIFFMANN, ELLIOTT
 ; APPLICANT: KRUTZCH, HENRY
 ; APPLICANT: MURATA, JUN
 ; TITLE OF INVENTION: AUTOTOXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
 ; TREATMENT: AUTOTOXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
 ; FILE REFERENCE: 2016-4149US4
 ; CURRENT APPLICATION NUMBER: US/09/483,631B
 ; CURRENT FILING DATE: 2000-01-17
 ; PRIORITY APPLICATION NUMBER: 07/822,043
 ; PRIORITY FILING DATE: 1992-01-17
 ; PRIORITY APPLICATION NUMBER: 08/2449,182
 ; PRIORITY FILING DATE: 1994-05-25
 ; PRIORITY APPLICATION NUMBER: 08/346,455
 ; PRIORITY FILING DATE: 1994-11-28
 ; PRIORITY APPLICATION NUMBER: 08/977,221
 ; PRIORITY FILING DATE: 1997-11-24
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 34
 ; LENGTH: 829
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Putative protein sequence of A2058 Autotoxin
 US-09-483-831B-34

Query Match Score 1964.5; DB 4; Length 829;
 Best Local Similarity 42.4%; Pred. No. 1.2e-182;
 Matches 363; Conservative 164; N mismatches 239; Indels 91; Gaps 10;

82 CWDFFDTCESTRWMCKNCRKCGTRELASLCSDDCLQKDKCDAKDYKSCVQGETSWL 141
 1 CHDFDELCKTARGWCTKDRGTYNEAACHSEDCLRGDCCTNYQVICKGBSHWVD 60

142 ENCDTAQOSOCOPREGFLPPLVIFSMGDGFREAYLTWDTLMPNINKLKTCGTHSKYRAMY 201
 61 DICEEKAACEPAGFPRPLIIFSVDGFRASYMKGSKMNPTEKLSCGTISPYRPVY 120

202 PTKTFPWNHYTIVTGlyPESHGIIIDNNMYDYNLNKNFSSLSSKEONNPawHGGOpMwLTAMY 261
 121 PTKTFPWNLYTATGlyPESHGIVGNSMDPFDATFHGREKENHRAWGGQLWLWATK 180

262 QGLKAKATYFWPGSEVIAINGSFPSPSYIMPYNGSVPFEERISTLKLWLDLPAKAERPRFYMF 321
 181 QSVKAGTFWV-----SVYPH-----ERRITLIRWLTLFDHERPSVAFYS 222

322 EPPDSCHAGGPVSA-----336

223 EQPDPSCHAGKYGFGPDESSYGSPPFTPKRKRKVKAPKRKRQERPVAPPKRKRKHRYDHY 282

337 -----RVTIALQVVDHAFRMNLMEGLKORNLENCAVNILLAHGMDDTYCNKNEYTDY 389
 283 AAETQRDKMTNPLRETDKIVGQLMGKLQKLRCCVNY_FVGDHGMEDYTCTRFELFSNY 342

390 PFRINFFYMEBPAPlR--AHHN_PHDFFSFNSEEIVNLNSCRKPDKHFKPLTPLPK 446
 343 LTNVDDTILVETGTLGRSKRSKESNNAYKD----KATIANLTCKKPDQHKYKLQHLPK 397

447 RLHYAKNVRIDKVLHVFDQW----LAVRSKSNTNC_GGGHGYNEFRSMEAFLAH 499
 398 RUYHANRRIEDHLLVERRHVARKPLDYKPGKCPFOGDHGFDNKVNMSMQTVFGY 457

500 GPSFKETEVPEPFENIEVYNUMLCDLRLIOPAPNNGTGSLNHLKVPFYEPHAEYSKF 559
 458 GPTEKYKIKVPPFENTELYNMCDLIGLKPAPNNGTGSLNHLRTINTFRPTIMEETVRP 517

560 SVEGRANFLPFTBSLDFC_PHQNSTOLEQYNOMLNQEETIAVKNLPEQRPRVYQK 618
 518 NYGMYLWQSDDLGCTCDKVEPKRNKLHTK---GSTEEHHLIGRPATYL 573

619 NVDHCLLHYREYVSGFQKAMMMPMSYYTVPQGDTSPLPPTPDCLRADVYPPSSQK 678
 574 -TRYDILYHTDESGSEIFMLLWNSYTSKQEEVSSYDPHITSVRDPVSPSSQN 632

679 CSYLAQKNNITGFLYPPASNRTSDQYDALTUNLWPMYEFKMMWDFHSTLLIHFAT 738
 633 CLAYKNDKOMSYGFLPFLPFLSSPEAKYDDEFLVNMVCPYTPAFAVNVYFORTLVCKAS 692

RESULT 14
 US-09-483-831B-34
 ; Sequence 34, Application US/09483831B
 ; Patent No. 641338
 ; GENERAL INFORMATION:
 ; APPLICANT: STRACKE, MARY
 ; APPLICANT: LICOTTA, LANCE
 ; APPLICANT: SCHIFFMANN, ELLIOTT
 ; APPLICANT: KRUTZCH, HENRY
 ; APPLICANT: MURATA, JUN
 ; TITLE OF INVENTION: AUTOTOXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
 ; TREATMENT: AUTOTOXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
 ; FILE REFERENCE: 2016-4149US4
 ; CURRENT APPLICATION NUMBER: US/09/483,631B
 ; CURRENT FILING DATE: 2000-01-17
 ; PRIORITY APPLICATION NUMBER: 07/822,043
 ; PRIORITY FILING DATE: 1992-01-17
 ; PRIORITY APPLICATION NUMBER: 08/2449,182
 ; PRIORITY FILING DATE: 1994-05-25
 ; PRIORITY APPLICATION NUMBER: 08/346,455
 ; PRIORITY FILING DATE: 1994-11-28
 ; PRIORITY APPLICATION NUMBER: 08/977,221
 ; PRIORITY FILING DATE: 1997-11-24
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 34
 ; LENGTH: 829
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Putative protein sequence of A2058 Autotoxin
 US-09-483-831B-34

Query Match Score 1964.5; DB 4; Length 829;
 Best Local Similarity 42.4%; Pred. No. 1.2e-182;
 Matches 363; Conservative 164; N mismatches 239; Indels 91; Gaps 10;

82 CWDFFDTCESTRWMCKNCRKCGTRELASLCSDDCLQKDKCDAKDYKSCVQGETSWL 141
 1 CHDFDELCKTARGWCTKDRGTYNEAACHSEDCLRGDCCTNYQVICKGBSHWVD 60

142 ENCDTAQOSOCOPREGFLPPLVIFSMGDGFREAYLTWDTLMPNINKLKTCGTHSKYRAMY 201
 61 DICEEKAACEPAGFPRPLIIFSVDGFRASYMKGSKMNPTEKLSCGTISPYRPVY 120

202 PTKTFPWNHYTIVTGlyPESHGIIIDNNMYDYNLNKNFSSLSSKEONNPawHGGOpMwLTAMY 261
 121 PTKTFPWNLYTATGlyPESHGIVGNSMDPFDATFHGREKENHRAWGGQLWLWATK 180

262 QGLKAKATYFWPGSEVIAINGSFPSPSYIMPYNGSVPFEERISTLKLWLDLPAKAERPRFYMF 321
 181 QSVKAGTFWV-----SVYPH-----ERRITLIRWLTLFDHERPSVAFYS 222

322 EPPDSCHAGGPVSA-----336

223 EQPDPSCHAGKYGFGPDESSYGSPPFTPKRKRKVKAPKRKRQERPVAPPKRKRKHRYDHY 282

337 -----RVTIALQVVDHAFRMNLMEGLKORNLENCAVNILLAHGMDDTYCNKNEYTDY 389
 283 AAETQRDKMTNPLRETDKIVGQLMGKLQKLRCCVNY_FVGDHGMEDYTCTRFELFSNY 342

390 PFRINFFYMEBPAPlR--AHHN_PHDFFSFNSEEIVNLNSCRKPDKHFKPLTPLPK 446
 343 LTNVDDTILVETGTLGRSKRSKESNNAYKD----KATIANLTCKKPDQHKYKLQHLPK 397

447 RLHYAKNVRIDKVLHVFDQW----LAVRSKSNTNC_GGGHGYNEFRSMEAFLAH 499
 398 RUYHANRRIEDHLLVERRHVARKPLDYKPGKCPFOGDHGFDNKVNMSMQTVFGY 457

500 GPSFKETEVPEPFENIEVYNUMLCDLRLIOPAPNNGTGSLNHLKVPFYEPHAEYSKF 559
 458 GPTEKYKIKVPPFENTELYNMCDLIGLKPAPNNGTGSLNHLRTINTFRPTIMEETVRP 517

560 SVEGRANFLPFTBSLDFC_PHQNSTOLEQYNOMLNQEETIAVKNLPEQRPRVYQK 618
 518 NYGMYLWQSDDLGCTCDKVEPKRNKLHTK---GSTEEHHLIGRPATYL 573

619 NVDHCLLHYREYVSGFQKAMMMPMSYYTVPQGDTSPLPPTPDCLRADVYPPSSQK 678
 574 -TRYDILYHTDESGSEIFMLLWNSYTSKQEEVSSYDPHITSVRDPVSPSSQN 632

679 CSYLAQKNNITGFLYPPASNRTSDQYDALTUNLWPMYEFKMMWDFHSTLLIHFAT 738
 633 CLAYKNDKOMSYGFLPFLPFLSSPEAKYDDEFLVNMVCPYTPAFAVNVYFORTLVCKAS 692

283 AATRODKMTNPRLREIDKIVGQIMDGKQKLKLRCCVNTIVGDHGMEDVTCRTEFLSNY 342
 QY 390 FPRINFFMYEGPAPRIR--AHHNIPHDFSSENSEEIVNLNSCRKPDQHFKPYLTPDLPK 446
 Db 343 LNUDDDTLIVPOTLGIRSFSNNKVD---EKAIIANITKPKDQHFKYLKQHLPK 397
 QY 447 RHYAKXNRVIDKVLFQWQ---LAVERSKEINTNCGGCNHGYNNERFSMEAIFLAH 499
 Db 398 RHYANTRIEDIHLVERRHVAEKPDLVYKKSFKCFQGDHGFDKRVNSMQTFVGY 457
 QY 500 GPSFEKTEVEPFENTEVYNYMCDLRLIOPAPNGTHGSLNLHULKVPEYEPSHAEVSKF 559
 Do 458 GPTFKTKVPPFENTELVNMCDLGLKEAPNGTHGSLNLHILRTNTFRPMPEEVTRP 517
 QY 560 SYCGFANPLPETSLDGFC-PHLQNSTOLPQEOYNONMLQEETATVKYNLPFGRPYTLQK 618
 Db 518 NPGIMYLQSDDDLGCTDDKEPKNKLDEALKHT---GSTEEBHLLYGRPAVLRY 573
 QY 619 NVDCHCLLYTHEYVSGESKGAKMMPMASSYTVPQLGDTSPLEPPTVPCDLRADYVPPSESQK 678
 Db 574 -TRYDILYHTDDESGSEIFMLMLTTSYTSKQAEVSSPDHHTSCVRDPVSPSPSQN 632
 QY 679 CSYFLADKNITIGELYAPPASNRRTSDQYDALITSNLVNMYYEFPKMDYFHSVLLJKHAT 738
 Db 633 CLAYNDKQMSYGFLLPPYLISSPAKYDAFLVTNMVPMVYPAKRVINYFQEVLVKRYAS 692
 QY 739 ERGVNTVSGPILFDYHYGHFDADEITHKLANTDVPIETHYFWVLTSCRNKSHTPENCP 798
 Db 693 ERGVNTVSGPILFDYDGLHDTEDKIKOYVEGSSIPVPTHYSIISNSCLDFTOPADKCD 752
 QY 799 GHLDVLPFIIPRPTNVESCPBEGRPEALVTEERTTAHARVDYELLTGDPYQDXVQPV 858
 Db 753 GPLSVSSSEFLPHRDPEECSNSSEDESKVVEELNMKHTARVDIRHEHTLSDFRKTSRSY 812
 QY 859 SEIQLQKTYLPLPFTETI 875
 Db 813 PAIILTKTYLTYSEI 829

RESULT 15
 PCT-US95-06613-34
 ; Sequence 34, Application PC/TUS9506613
 ; GENERAL INFORMATION:
 ; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
 ; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTSCH,
 ; APPLICANT: HENRY; MURATA, JUN
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; NUMBER OF SEQUENCES: 69
 ; ADDRESSSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06613
 ; FILING DATE: 24-MAY-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/346,455
 ; FILING DATE: 28-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249,182
 ; FILING DATE: 25-MAY-1994
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/822,043
 ; FILING DATE: 17-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DOROTHY R. AUTH
 ; REFERENCE/DOCKET NUMBER: 36-434
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 829
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Protein
 ; HYPOTHETICAL: No
 ; ORIGINALE SOURCE:
 ; ORGANISM: Human
 ; STRAIN:
 ; INDIVIDUAL ISOLATE:
 ; DEVELOPMENTAL STAGE:
 ; HAPLOTYPE:
 ; TISSUE TYPE:
 ; CELL TYPE: Melanoma
 ; CELL LINE: A2058
 ; ORIGINELLE:
 ; FEATURE:
 ; LOCATION:
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION: Putative Protein
 ; OTHER INFORMATION: sequence of A2058 Autotaxin
 ; PCT-US95-06613-34

Query Match 40.9%; Score 1964.5; DB 5; Length 829;
 Best Local Similarity 42.4%; Pred. No. 1-2e-182;
 Matches 363; Conservative 164; Mismatches 239; Indels 91; Gaps 10;

Qy 82 CWDFFDTCVESTRIWMNKERKPCGETRLEASLSCSDCLQKDCCADYKSVQGETSWLE 141
 Db 1 CHDFDECLKTYARGNECTKDRGEVNEENACHCSEDCLRGDCCTNYQVICKGEHWVD 60
 Qy 142 ENCDTADQSOCPGEGFDLPPVLFMSDGFRAEYLWTDDTMPINTKLCGTHSKYRMAY 201
 Db 61 DCEEBIAECAGFVRPLIFSVDFGFRASYMKGSKMPNIEKLRCGTSYPMRPy 120
 Qy 202 PTKTFPHYHTVTLGPESHGITIONNMKVDNLNKNSLSKSEONNPWMEGPMLTAMY 261
 Db 221 PTKTFPHLYTATGGLYPPESGIVGNSMIDPVFDATFHGRGREFENHRWGGPLWITAK 180
 Qy 262 QGKAAATYFWPGSEVAINGSFPSLYMPYNGSVPPFEERSTULLKWLDPKAERFRFTMYF 321
 Db 281 QGVKAGTFFW-----SVVPH-----ERRLTIRWLTDHERPSVTAFY 222
 Qy 322 EBPDSSHAGGPVSA-----
 Db 223 EQPDFSSHKTYGPGDESSYGSPTPARKRQEEREVAPPKRERKRRKIHMDHY 282
 Qy 337 -----RVIKALQVYDHAFGQMLMEGLIKORNHLNCVNILLADHGMDQTYCNKMEYMDY 389
 Db 283 AAETRQKMTNPLREDIKTVGQMDGLKOLKERCVNTYFVBGHDGMDDVTCDRTEPLSY 342
 Qy 390 FPRINFFYMEGPAPIR--AHNIPHDEFFSENSEEVYRNLSCKRKPDQHFKPYLTPDLPK 446
 Db 343 LTNVDDDTLVEGLGRISRSFSNNAKYD----PKAIANLTKCPQHFKPYLKQHLPK 397
 Qy 447 RLHYAKXNRVIDKVLFQWQ---LAVERSKEINTNCGGCNHGYNNERFSMEAIFLAH 499
 Db 398 RLHYANTRIEDIHLVERRHVAEKPDLVYKKSFKCFQGDHGFDKRVNSMQTFVGY 457
 Qy 500 GPSFEKTEVEPFENIEVYNLMDLRLIOPAPNGTHGSLNLHULKVPEYEPSHAEVSKF 559

Search completed: July 6, 2004, 13:21:04
Job time : 27 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:19:53 ; Search time 56 Seconds

(without alignments)

4863.810 Million cell updates/sec

Title: US-10-005-480A-743

Perfect score: 4804

Sequence: 1 MESTIILATEQPVKNTLKK.....QPVSEIIQLKTYLPTFETTI 875

Scoring table: BL05062

GapOp 10.0 , Gapext 0.5

Searched: 1276550 seqs, 311283816 residues

Total number of hits satisfying chosen parameters:

1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Established Applications API: *

1: /cgns_6_ptodata/2/pubbaa/US07_PUBCOMB.pep:*

2: /cgns_6_ptodata/2/pubbaa/PCN_NEW_PUB.pep:*

3: /cgns_6_ptodata/2/pubbaa/US06_NEW_PUB.pep:*

4: /cgns_6_ptodata/2/pubbaa/US06_PUBCOMB.pep:*

5: /cgns_6_ptodata/2/pubbaa/US07_NEW_PUB.pep:*

6: /cgns_6_ptodata/2/pubbaa/PCNS_PUBCOMB.pep:*

7: /cgns_6_ptodata/2/pubbaa/US08_PUBCOMB.pep:*

8: /cgns_6_ptodata/2/pubbaa/US09_PUBCOMB.pep:*

9: /cgns_6_ptodata/2/pubbaa/US09_E_PUBCOMB.pep:*

10: /cgns_6_ptodata/2/pubbaa/US09C_PUBCOMB.pep:*

11: /cgns_6_ptodata/2/pubbaa/US09C_N_PUBCOMB.pep:*

12: /cgns_6_ptodata/2/pubbaa/US10_A_PUBCOMB.pep:*

13: /cgns_6_ptodata/2/pubbaa/US10_B_PUBCOMB.pep:*

14: /cgns_6_ptodata/2/pubbaa/US10_C_PUBCOMB.pep:*

15: /cgns_6_ptodata/2/pubbaa/US10_N_PUB.pep:*

16: /cgns_6_ptodata/2/pubbaa/US60_NEW_PUB.pep:*

17: /cgns_6_ptodata/2/pubbaa/US60_PUBCOMB.pep:*

18: /cgns_6_ptodata/2/pubbaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 4804 100.0 875 14 US-10-062-109A-743 Sequence 743, App

2 4804 100.0 875 14 US-10-062-109A-747 Sequence 747, App

3 4804 100.0 875 14 US-10-062-109A-751 Sequence 751, App

4 4804 100.0 875 14 US-10-005-480A-743 Sequence 743, App

5 4804 100.0 875 14 US-10-005-480A-747 Sequence 747, App

6 4804 100.0 875 14 US-10-005-480A-751 Sequence 751, App

7 4804 100.0 875 15 US-10-291-241-3 Sequence 3, App

8 4804 100.0 875 15 US-10-291-241-11 Sequence 11, App

9 4804 100.0 875 15 US-10-291-241-16 Sequence 16, App

10 4804 100.0 875 15 US-10-291-241-21 Sequence 21, App

11 4804 100.0 875 15 US-10-291-241-22 Sequence 22, App

12 4804 100.0 875 15 US-10-291-241-81 Sequence 81, App

13 4804 100.0 875 15 US-10-291-241-94 Sequence 94, App

14 4804 100.0 875 15 US-10-291-241-95 Sequence 95, App

15 4804 100.0 875 15 US-10-291-241-96 Sequence 96, App

ALIGNMENTS

RESULT 1 US-10-062-109A-743

; Sequence 743, Application US/10062109A

; Publication No. US20030165505A1

; GENERAL INFORMATION:

; APPLICANT: Agensys

; APPLICANT: Challita-Eld, Pia M.

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Paris, Mary

; APPLICANT: Hubert, Rene S.

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Ayala

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

; TITLE OF INVENTION: Entitled 161P210B Useful in Treatment and Detection of

; TITER OF INVENTION: Cancer

; FILE REFERENCE: 51158-20062-01

; CURRENT APPLICATION NUMBER: US/10/062-109A

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: US 10/005,480

; NUMBER OF SEQ ID NOS: 765

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 743

; LENGTH: 875

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-062-109A-743

Query Match 100.0%; Score 4804; DB 14; Length 875;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0;

Matches 875; Conservative 0; Gaps 0;

Y Q 1 MESTLTLATEQPVKNTLKKYACIVLALIVMSLGIGLGLGLRKEQSKRCKFCFD 60

Db 1 MESTLTLATEQPVKNTLKKYACIVLALIVMSLGIGLGLGLRKEQSKRCKFCFD 60

Qy 61 ASPGLENCRCDVACKDRGDCMDFFCTVESTRIMCNKPFRCGETLEASLCSCSDCL 120

61 ASFRGLENCRCVDACKDRGDCWDFFDTCEVSTRIWMCNKFRCGETRLASLCSDDDL 120 ; PRIOR APPLICATION NUMBER: US 10/005, 480
 Qy 121 QKKDCCADYKSYCOGETSWLEENCDTAQOSOCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180 ; PRIOR FILING DATE: 2001-11-07
 Pb 121 QKKDCCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180 ; NUMBER OF SEQ ID NOS: 765
 Software: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 747
 ; LENGTH: 875
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-062-109A-747

Query Match	Score	DB 14;	Length	875;
Best Local Similarity	100 %			
Matches	875;	Conservative	0;	Missmatches 0; Indels 0; Gaps 0;
Qy	1	MESTLTLATEOPVKCNTLKKEYKIAIVLLAVIMSLIGLGLGIRKLKGSGCRKCPD 60		
Db	1	MESTLTLATEOPVKCNTLKKEYKIAIVLLAVIMSLIGLGLGIRKLKGSGCRKCPD 60		
Qy	61	ASFRGLENCRCVDACKDRGDCWDFFDTCEVSTRIWMCNKFRCGETRLASLCSDDDL 120		
Db	61	ASFRGLENCRCVDACKDRGDCWDFFDTCEVSTRIWMCNKFRCGETRLASLCSDDDL 120		
Qy	121	QRKDCCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180		
Db	121	QRKDCCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180		
Qy	121	QKKDCCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180		
Db	121	QKKDCCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDTL 180		
Qy	121	MPNINKLDPKAERPREFTYMFEEPDSSGHAGGPVSARVTKALQVVDHAFGMLMEGLKORN 360		
Db	121	MPNINKLDPKAERPREFTYMFEEPDSSGHAGGPVSARVTKALQVVDHAFGMLMEGLKORN 360		
Qy	121	LNANCNTILLADHGMDQTCNKRMEMTDFPRINFTYMEGAPRIRAHNIPHDFFNS 420		
Db	121	LNANCNTILLADHGMDQTCNKRMEMTDFPRINFTYMEGAPRIRAHNIPHDFFNS 420		
Qy	121	EEIVRNLSCKRPDKDHFKPYLTDPDLPKRLHYAKNVRIDKTHLYFDQOQLAVERSKSNTNGC 480		
Db	121	EEIVRNLSCKRPDKDHFKPYLTDPDLPKRLHYAKNVRIDKTHLYFDQOQLAVERSKSNTNGC 480		
Qy	121	4.21 BEIVRNLSCKRPDKDHFKPYLTDPDLPKRLHYAKNVRIDKTHLYFDQOQLAVERSKSNTNGC 480		
Db	121	4.21 BEIVRNLSCKRPDKDHFKPYLTDPDLPKRLHYAKNVRIDKTHLYFDQOQLAVERSKSNTNGC 480		
Qy	121	GNHGYNNERFSMEAIAFLAHPGSFKEKTEVEPFENIEVNLMCDLLRQAPANGTHGSLN 540		
Db	121	GNHGYNNERFSMEAIAFLAHPGSFKEKTEVEPFENIEVNLMCDLLRQAPANGTHGSLN 540		
Qy	121	541 HLLKYPFPDSHAEVSKSVCFANPLPTESDLCFCPHQLNSTOLEQVNQMLNLTQEETI 600		
Db	121	541 HLLKYPFPDSHAEVSKSVCFANPLPTESDLCFCPHQLNSTOLEQVNQMLNLTQEETI 600		
Qy	121	601 TATYKVNLIFGRPFLQVNVDHCLLYHREYVSGFKAMPMWSSTVQPLQGDTSPLPPT 660		
Db	121	601 TATYKVNLIFGRPFLQVNVDHCLLYHREYVSGFKAMPMWSSTVQPLQGDTSPLPPT 660		
Qy	121	661 VPDLRRADVRPSEQSOKCSFYLADKNITTHGFLYPPASNRTSDSQDALITSNLYVMYE 720		
Db	121	661 VPDLRRADVRPSEQSOKCSFYLADKNITTHGFLYPPASNRTSDSQDALITSNLYVMYE 720		
Qy	121	721 FRKWDYTHPSVLLJKHATERGUNIVSGPEDIYNYDCHEDADDETKHLANTDVPDPTH 780		
Db	121	721 FRKWDYTHPSVLLJKHATERGUNIVSGPEDIYNYDCHEDADDETKHLANTDVPDPTH 780		
Qy	781	FVVLTSCKNSKHTPENCPGMDLVPLFPIPHRTNVSCPEKGPKPEALWVEBFTAHAYR 840		
Db	781	FVVLTSCKNSKHTPENCPGMDLVPLFPIPHRTNVSCPEKGPKPEALWVEBFTAHAYR 840		
Qy	781	DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875		
Db	781	DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875		
Qy	841	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875		
Db	841	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875		
Qy	601	TATYKNULPGRRVLOQVNVDLFLYREYVSGFKAMPMWSSTVQPLQGDTSPLPPT 660		
Db	601	TATYKNULPGRRVLOQVNVDLFLYREYVSGFKAMPMWSSTVQPLQGDTSPLPPT 660		
Qy	661	VPDCLRADVRPSEQSOKCSFYLADKNITTHGFLYPPASNRTSDSQDALITSNLYVMYE 720		
Db	661	VPDCLRADVRPSEQSOKCSFYLADKNITTHGFLYPPASNRTSDSQDALITSNLYVMYE 720		
Qy	721	721 FROMWDYTHPSVLLJKHATERGUNIVSGPIDIYNYTDGHFDADDETKHLANTDVPDPTH 780		
Db	721	721 FROMWDYTHPSVLLJKHATERGUNIVSGPIDIYNYTDGHFDADDETKHLANTDVPDPTH 780		
Qy	661	661 VPDCLRADVRPSEQSOKCSFYLADKNITTHGFLYPPASNRTSDSQDALITSNLYVMYE 720		
Db	661	661 VPDCLRADVRPSEQSOKCSFYLADKNITTHGFLYPPASNRTSDSQDALITSNLYVMYE 720		
Qy	841	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875		
Db	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875			
Qy	841	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875		
Db	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875			
Qy	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875			
Db	841 DVLLTGIDFYQDVQPVSEIIOLQKLYLPTFETTI 875			

RESULT 2
 US-10-062-109A-747
 Sequence 747, Application US/10062109A
 Publication No. US20030165505A1
 GENERAL INFORMATION:
 APPLICANT: Agensys
 APPLICANT: Challita-Eld, Pia M.
 APPLICANT: Raitano, Arthur B.
 APPLICANT: Paris, Mary
 APPLICANT: Huber, Rene S.
 APPLICANT: Morrison, Karen Jane Meyrick
 APPLICANT: Jakobovits, Ayu
 TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 51158-20062-01
 CURRENT APPLICATION NUMBER: US/10/062,109A
 CURRENT FILING DATE: 2002-01-31

RESULT 3									
US-10-062-109A-751 Sequence 751, Application US/10062109A									
; GENERAL INFORMATION:									
;	APPLICANT: Agensys	;	;	;	;	;	;	;	;
;	APPLICANT: Challita-Bid, Pia M.	;	;	;	;	;	;	;	;
;	APPLICANT: Raitano, Arthur B.	;	;	;	;	;	;	;	;
;	APPLICANT: Paris, Mary	;	;	;	;	;	;	;	;
;	APPLICANT: Hubert, Rene S.	;	;	;	;	;	;	;	;
;	APPLICANT: Morrison, Karen Jane Meyrick	;	;	;	;	;	;	;	;
;	APPLICANT: Jakobovits, Ayra	;	;	;	;	;	;	;	;
;	TITLE OF INVENTION: Nucleic Acid and Corresponding Protein	;	;	;	;	;	;	;	;
;	TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of	;	;	;	;	;	;	;	;
;	TITLE OF INVENTION: Cancer	;	;	;	;	;	;	;	;
;	FILE REFERENCE: 51158-20052-01	;	;	;	;	;	;	;	;
;	CURRENT APPLICATION NUMBER: US/10/062,109A	;	;	;	;	;	;	;	;
;	CURRENT FILING DATE: 2002-01-31	;	;	;	;	;	;	;	;
;	PRIOR APPLICATION NUMBER: US 10/005,480	;	;	;	;	;	;	;	;
;	PRIOR FILING DATE: 2001-11-07	;	;	;	;	;	;	;	;
;	NUMBER OF SEQ ID NOS: 765	;	;	;	;	;	;	;	;
;	SOFTWARE: FastSeq for Windows Version 4.0	;	;	;	;	;	;	;	;
;	SEQ ID NO: 751	;	;	;	;	;	;	;	;
;	LENGTH: 875	;	;	;	;	;	;	;	;
;	TYPE: PRT	;	;	;	;	;	;	;	;
;	ORGANISM: Homo sapiens	;	;	;	;	;	;	;	;
US-10-062-109A-751									
;	Query Match Score 4804; DB 14; Length 875;	;	;	;	;	;	;	;	;
;	Best Local Similarity 100.0%; Pred. No. 0;	;	;	;	;	;	;	;	;
;	Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	;	;	;	;	;	;	;	;
Qy	1 MESTIILATEQPVKNTLKKYKIACTVLLVLLVMSIGLGLGIRKLEQGSCRKCFD	60	;	;	;	;	;	;	;
Db	1 MESTIILATEQPVKNTLKKYKIACTVLLVLLVMSIGLGLGIRKLEQGSCRKCFD	60	;	;	;	;	;	;	;
Qy	61 ASFRGLENCRCDVACKDRGDCCWDFDTCYESTRMCNKFRGGETRLESLSLCSSDDCL	120	;	;	;	;	;	;	;
Db	61 ASFRGLENCRCDVACKDRGDCCWDFDTCYESTRMCNKFRGGETRLESLSLCSSDDCL	120	;	;	;	;	;	;	;
Qy	121 QKKDCCADYKSVCQGFTSWLBENCDTAQOQSOCPEGFIDLPVTFESMDGFAEYLTYWDTL	180	;	;	;	;	;	;	;
Db	121 QKKDCCADYKSVCQGFTSWLBENCDTAQOQSOCPEGFIDLPVTFESMDGFAEYLTYWDTL	180	;	;	;	;	;	;	;
Qy	181 MPNINKLKTGCIHSKMRAMYPTKTFPNHYTTIVGYPESHGIIIDNNMNDYVLNKNFNSL	240	;	;	;	;	;	;	;
Db	181 MPNINKLKTGCIHSKMRAMYPTKTFPNHYTTIVGYPESHGIIIDNNMNDYVLNKNFNSL	240	;	;	;	;	;	;	;
Qy	241 SKEQNPAWHEQGPWMLTANYQGLKATYWPGEVAINGSFSPSYMPYNGSVPERIS	300	;	;	;	;	;	;	;
Db	241 SKEQNPAWHEQGPWMLTANYQGLKATYWPGEVAINGSFSPSYMPYNGSVPERIS	300	;	;	;	;	;	;	;
Qy	301 TLLKNDLPLKPERPRYTMPEPDPSGHICGPVSVARIALQVDAHGMLMEGIKQRN	360	;	;	;	;	;	;	;
Db	301 TLLKNDLPLKPERPRYTMPEPDPSGHICGPVSVARIALQVDAHGMLMEGIKQRN	360	;	;	;	;	;	;	;
Qy	361 LHNCVNITILLADHGMCQTYCNKMEYMTDYFPRIINFYMYEGPAPTRANTPHDFFSFNS	420	;	;	;	;	;	;	;
Db	361 LHNCVNITILLADHGMCQTYCNKMEYMTDYFPRIINFYMYEGPAPTRANTPHDFFSFNS	420	;	;	;	;	;	;	;
Qy	421 EBI1VRNLSCRDPDQHKPKLTPLDPLPRLHYAKNVRDKVHLFVDQQLWLRSKSNNTNGG	480	;	;	;	;	;	;	;
Db	421 EBI1VRNLSCRDPDQHKPKLTPLDPLPRLHYAKNVRDKVHLFVDQQLWLRSKSNNTNGG	480	;	;	;	;	;	;	;
Qy	481 GHNGTNEPFSMEAFLAHGPKSFKEKTEVEPFENIYVNMCDLRLIQAPNNNGHGSLN	540	;	;	;	;	;	;	;
Db	481 GHNGTNEPFSMEAFLAHGPKSFKEKTEVEPFENIYVNMCDLRLIQAPNNNGHGSLN	540	;	;	;	;	;	;	;
Qy	541 HLLKVFEYEPHAEVSKESVCGFANPLPTESLDCCPHLONSTQLEQVQMLNLTQEEL	600	;	;	;	;	;	;	;
Db	541 HLLKVFEYEPHAEVSKESVCGFANPLPTESLDCCPHLONSTQLEQVQMLNLTQEEL	600	;	;	;	;	;	;	;

Qy	601	TATVKNLPGFRPRFLQRNVDHCLLYREYVSGGKARMPMSSYTSQLDTPSLPPT	660
Db	601	TATVKNLPGFRPRFLQRNVDHCLLYREYVSGGKARMPMSSYTSQLDTPSLPPT	660
Qy	661	VPDCILRADVRPPSEQKCSPLAKNITHGFLYPASRRTSDQYDALITSNLVPWYEB	720
Db	661	VPDCILRADVRPPSEQKCSPLAKNITHGFLYPASRRTSDQYDALITSNLVPWYEB	720
Qy	721	FRKMWDYFHSVLLIKHATERGVNVTVSGPFLDNYDGHFDADPDETKHLANTDVP	780
Db	721	FRKMWDYFHSVLLIKHATERGVNVTVSGPFLDNYDGHFDADPDETKHLANTDVP	780
Qy	781	FVLLTSCKNSKSHTPENCPGMWDLVLETFIPIRPTNVESCEPGKPPALWTEERFAHIAFVR	840
Db	781	FVLLTSCKNSKSHTPENCPGMWDLVLETFIPIRPTNVESCEPGKPPALWTEERFAHIAFVR	840
Qy	841	DYBLLTGDFDQDKVQPVSEILQLRTYLPTFETAI	875
Db	841	DYBLLTGDFDQDKVQPVSEILQLRTYLPTFETAI	875
Qy	841	DYBLLTGDFDQDKVQPVSEILQLRTYLPTFETAI	875
Db	841	DYBLLTGDFDQDKVQPVSEILQLRTYLPTFETAI	875
RESULT 4			
US-10-005-480A-743			
; Sequence 743, Application US/10005480A			
; GENERAL INFORMATION:			
; APPLICANT: Agensys			
; APPLICANT: Chaillita-Bid, Pia M.			
; APPLICANT: Raitano, Arthur B.			
; APPLICANT: Paris, Mary			
; APPLICANT: Hubert, Rene S.			
; APPLICANT: Morrison, Karen Jane Meyrick			
; APPLICANT: Jakobovits, AyA			
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein			
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of			
; TITLE OF INVENTION: Cancer			
; FILE REFERENCE: 51158-20062.00			
; CURRENT APPLICATION NUMBER: US10/005,480A			
; CURRENT FILING DATE: 2001-11-07			
; NUMBER OF SEQ ID NOS: 765			
; SOFTWARE: asaseq For Windows Version 4.0			
; SEQ ID NO: 743			
; LENGTH: 875			
; TYPE: PRT			
; ORGANISM: Homo Sapien			
; US-10-005-480A-743			
Query Match Score 4804; DB 14; Length 875;			
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;			
Matches 875; Conservative 100.0%;			
1 MESTLTATEQPVKONTLKKYKIACTIVLALLVIMSLGLGLGLRKLEKGCSRKRKCFD 60			
1 MESTLTATEQPVKONTLKKYKIACTIVLALLVIMSLGLGLGLRKLEKGCSRKRKCFD 60			
61 ASRGLENCRCDVACKDRGDCWDDTCTVSTRWMCNKFRCGCCTRLASLCSCDDCL 120			
61 ASRGLENCRCDVACKDRGDCWDDTCTVSTRWMCNKFRCS3TRLASLCSCDDCL 120			
121 OKEDCCADYKSVCOGETSMILENCDTAQSQCPCFDLPPVILEMSDGFRAEYLTYWTDTL 180			
121 QKEDCCADYKSVCOGETSMILENCDTAQSQCPCFDLPPVILEMSDGFRAEYLTYWTDTL 180			
181 MPNINKLKTKGTHSKYMRAMPTKPFNHYTIVTGYPESHGIDNNMYDNLNKNSLS 240			
181 MPNINKLKTKGTHSKYMRAMPTKPFNHYTIVTGYPESHGIDNNMYDNLNKNSLS 240			
241 SKEQNNPAWHQWHPQMMIATMQLKATYWPGSVAINGSFPSLYMPNGSYFPEERTS 300			
241 SKEQNNPAWHQWHPQMMIATMQLKATYWPGSVAINGSFPSLYMPNGSYFPEERTS 300			
301 TJKWLDPKAERPRFTYMFPEEPDSGHAGGPVSARVIKALQWHDAGFMMEGLKORN 360			

FILE REFERENCE: 51158-20062 00
 CURRENT APPLICATION NUMBER: US/10/005,480A
 NUMBER OF SEQ ID NCS: 765
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 751
 LENGTH: 875
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-005-480A-751

Query Match 100.0%; Score 4804; DB 14; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 875; Conservative 0;

Qy 1 MESTLTLATEQPVRNTLKKYKACIVLLALIVMSIGLGLGKRLKEKGSCRXKCFD 60
 Db 1 MESTLTLATEQPVRNTLKKYKACIVLLALIVMSIGLGLGKRLKEKGSCRXKCFD 60

Qy 61 ASFRGLENCRCDYACKDGDCCDFEDTCVESTRWNCKFGEIRLEASICSCDDCL 120
 Db 61 ASFRGLENCRCDYACKDGDCCDFEDTCVESTRWNCKFGEIRLEASICSCDDCL 120

Qy 121 QKEDCCADAKYSVCOGETSWLEENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLWTDTL 180
 Db 121 QKEDCCADAKYSVCOGETSWLEENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLWTDTL 180

Qy 181 MPNINKLKCIGHSKYMAMYPIKTFPHHYTIVTGLYPSHGLIDNMVDLNKNFSL 240
 Db 181 MPNINKLKCIGHSKYMAMYPIKTFPHHYTIVTGLYPSHGLIDNMVDLNKNFSL 240

Qy 241 SKENONPAWHPGOMMLAMYQGIKAATYFWPOSEEAVINGSFSIIMPYNGVPFEIR 300
 Db 241 SKENONPAWHPGOMMLAMYQGIKAATYFWPOSEEAVINGSFSIIMPYNGVPFEIR 300

Qy 301 TIKWLDDLPKAERPRFYTMFEEPDSSHAGGPVSARYVKAQVYDHAFGMIMEGIKORN 360
 Db 301 TIKWLDDLPKAERPRFYTMFEEPDSSHAGGPVSARYVKAQVYDHAFGMIMEGIQRN 360

Qy 361 LHCYCNVILLADHGMQTYCNCMEYMTDXPRINFYMEGAPRRAHNIPHDFFESNS 420
 Db 361 LHCYCNVILLADHGMQTYCNCMEYMTDXPRINFYMEGAPRRAHNIPHDFFESNS 420

Qy 421 EE1TRNLSCRKPDKPKYLTPDLPKRLYAKNRIDTHLFDQQAIVRKSNNTNGG 480
 Db 421 EE1TRNLSCRKPDKPKYLTPDLPKRLYAKNRIDTHLFDQQAIVRKSNNTNGG 480

Qy 481 GNGHYNNEFRSMEAFLAHPGSFKEKTYEPFENIEVNLMCDLURCPAPNGTHESSLN 540
 Db 481 GNGHYNNEFRSMEAFLAHPGSFKEKTYEPFENIEVNLMCDLURCPAPNGTHESSLN 540

Qy 541 HLLKVPFYEFYSHAEEVKSFVCGPANPLPTESLDCECPHLQNTOLEYNOMLNQEII 600
 Db 541 HLLKVPFYEFYSHAEEVKSFVCGPANPLPTESLDCECPHLQNTOLEYNOMLNQEII 600

Qy 601 TATVKCNLPGCRPRVLUQNDVHCLJYRREYSGEGKAMMPMSSSYTPOGLDTSPPLPT 660
 Db 601 TATVKCNLPGCRPRVLUQNDVHCLJYRREYSGEGKAMMPMSSSYTPOGLDTSPPLPT 660

Qy 661 VPDCLRADYVPPSESQKSFLADKNTFHGLYPPASNRTSDOYDALITSULVPMYEE 720
 Db 661 VPDCLRADYVPPSESQKSFLADKNTFHGLYPPASNRTSDOYDALITSULVPMYEE 720

Qy 721 FRKMDYFHSVLLKHAETBNGVAVSGPLFDNYDGHEDAPDBTKHLANTDVPIPPY 780
 Db 721 FRKMDYFHSVLLKHAETBNGVAVSGPLFDNYDGHEDAPDBTKHLANTDVPIPPY 780

Qy 781 FVVLTSCKNSKHTPENCPGWLDVLPFIIPHRTNVYESCPGKPEALWBEERTAHIAVVR 840
 Db 781 FVVLTSCKNSKHTPENCPGWLDVLPFIIPHRTNVYESCPGKPEALWBEERTAHIAVVR 840

Qy 841 DVEJLTGDLDFYQDQVPSVSEILQLKTYLPTFETTI 875

Db 841 DVEJLTGDLDFYQDQVPSVSEILQLKTYLPTFETTI 875

RESULT 7
 US-10-2901-241-3
 Sequence 3, Application US/10291241
 Publication No. US20030206905A1

GENERAL INFORMATION:
 / APPLICANT: Agensys, Inc.
 / Publication: Robert Kendall Morrison
 / APPLICANT: Arthur B. Raitano
 / APPLICANT: Mary Paris
 / APPLICANT: Rene S. Hubert
 / APPLICANT: Wanomao Ge
 / APPLICANT: Karen Jane Mayrick Morrison
 / APPLICANT: Pia M. Challal-Eid
 / TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 / TITLE OF INVENTION: ENTILLED 161PPF10B USEFUL IN TREATMENT AND DETECTION OF
 / TITLE OF INVENTION: CANCER
 / FILE REFERENCE: 51158-20062-20
 / CURRENT APPLICATION NUMBER: US/10/291,241
 / CURRENT FILING DATE: 2003-03-18
 / PRIOR APPLICATION NUMBER: US 10/005,480
 / PRIOR FILING DATE: 2001-11-07
 / PRIOR APPLICATION NUMBER: US 10/062,109
 / PRIOR FILING DATE: 2002-01-31
 / PRIOR APPLICATION NUMBER: US 60/282,739
 / PRIOR FILING DATE: 2001-04-10
 / NUMBER OF SEQ ID NOS: 103
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 3
 / LENGTH: 875
 / TYPE: PRT
 / ORGANISM: Homo Sapiens

US-10-291-241-3

Query Match 100.0%; Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 875; Conservative 0;

Qy 1 MESTLTLATEQPVKNTLKEYKIAIVLAVLIVMSIGLGLGKRLKEKGSCRKCFD 60
 Db 1 MESTLTLATEQPVKNTLKEYKIAIVLAVLIVMSIGLGLGKRLKEKGSCRKCFD 60

Qy 61 ASFRGLENCRCDVACKDGDCCDFEDTCVESTRWNCKFGEIRLEASICSCDDCL 120
 Db 61 ASFRGLENCRCDVACKDGDCCDFEDTCVESTRWNCKFGEIRLEASICSCDDCL 120

Qy 61 ASFRGLENCRCDVACKDGDCCDFEDTCVESTRWNCKFGEIRLEASICSCDDCL 120
 Db 61 ASFRGLENCRCDVACKDGDCCDFEDTCVESTRWNCKFGEIRLEASICSCDDCL 120

Qy 121 QKEDCCADAKYSVCOGETSWLEENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLWTDTL 180
 Db 121 QKEDCCADAKYSVCOGETSWLEENCDTAQSQCPEGFDLPPVILFSMDGFRAEYLWTDTL 180

Qy 181 MPNINKLKCIGHSKYMAMYPIKTFPHHYTIVTGLYPSHGLIDNMVDLNKNFSL 240
 Db 181 MPNINKLKCIGHSKYMAMYPIKTFPHHYTIVTGLYPSHGLIDNMVDLNKNFSL 240

Qy 241 SKENONPAWHPGOMMLAMYQGIKAATYFWPOSEEAVINGSFSIIMPYNGVPFEIR 300
 Db 241 SKENONPAWHPGOMMLAMYQGIKAATYFWPOSEEAVINGSFSIIMPYNGVPFEIR 300

Qy 301 TIKWLDDLPKAERPRFYTMFEEPDSSHAGGPVSARYVKAQVYDHAFGMIMEGIKORN 360
 Db 301 TIKWLDDLPKAERPRFYTMFEEPDSSHAGGPVSARYVKAQVYDHAFGMIMEGIQRN 360

Qy 361 LHCYCNVILLADHGMQTYCNCMEYMTDXPRINFYMEGAPRRAHNIPHDFFESNS 420
 Db 361 LHCYCNVILLADHGMQTYCNCMEYMTDXPRINFYMEGAPRRAHNIPHDFFESNS 420

Qy 421 EE1TRNLSCRKPDKPKYLTPDLPKRLYAKNRIDTHLFDQQAIVRKSNNTNGG 480
 Db 421 EE1TRNLSCRKPDKPKYLTPDLPKRLYAKNRIDTHLFDQQAIVRKSNNTNGG 480

Qy 481 GNGHYNNEFRSMEAFLAHPGSFKEKTYEPFENIEVNLMCDLURCPAPNGTHESSLN 540
 Db 481 GNGHYNNEFRSMEAFLAHPGSFKEKTYEPFENIEVNLMCDLURCPAPNGTHESSLN 540

Qy 541 HLLKVPFYEFYSHAEEVKSFVCGPANPLPTESLDCECPHLQNTOLEYNOMLNQEII 600
 Db 541 HLLKVPFYEFYSHAEEVKSFVCGPANPLPTESLDCECPHLQNTOLEYNOMLNQEII 600

Qy 601 TATVKCNLPGCRPRVLUQNDVHCLJYRREYSGEGKAMMPMSSSYTPOGLDTSPPLPT 660
 Db 601 TATVKCNLPGCRPRVLUQNDVHCLJYRREYSGEGKAMMPMSSSYTPOGLDTSPPLPT 660

Qy 661 VPDCLRADYVPPSESQKSFLADKNTFHGLYPPASNRTSDOYDALITSULVPMYEE 720
 Db 661 VPDCLRADYVPPSESQKSFLADKNTFHGLYPPASNRTSDOYDALITSULVPMYEE 720

Qy 721 FRKMDYFHSVLLKHAETBNGVAVSGPLFDNYDGHEDAPDBTKHLANTDVPIPPY 780
 Db 721 FRKMDYFHSVLLKHAETBNGVAVSGPLFDNYDGHEDAPDBTKHLANTDVPIPPY 780

Qy 781 FVVLTSCKNSKHTPENCPGWLDVLPFIIPHRTNVYESCPGKPEALWBEERTAHIAVVR 840
 Db 781 FVVLTSCKNSKHTPENCPGWLDVLPFIIPHRTNVYESCPGKPEALWBEERTAHIAVVR 840

Qy 841 DVEJLTGDLDFYQDQVPSVSEILQLKTYLPTFETTI 875

RESULT 8

US-10-291-241-11
 Sequence 11, Application US/10291241
 Publication No. US20030206905A1
 GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Faris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Pia M. Chaillita-Bid
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
 ; TITLE OF INVENTION: CANCER
 FILE REFERENCE: 51158-20062-20
 CURRENT APPLICATION NUMBER: 2003-10/291-241
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/005,480
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 10/062,109
 PRIOR FILING DATE: 2002-01-31
 PRIOR APPLICATION NUMBER: US 60/282,739
 NUMBER OF SEQ ID NOS: 103
 SEQ ID NO: 11
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-291-241-11

Query Match Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESTLTLATEOPVKNTLTKYKIACTVLLAVIMSLGLGLGLGRKLGKQGSRKKCFD 60
 Db 1 MESTLTLATEOPVKNTLTKYKIACTVLLAVIMSLGLGLGLGRKLGKQGSRKKCFD 60
 Qy 61 ASFRGLENCRCVDACKDRGDCWDFFEDTCVESTRIWMCNKFERGEBTRLEASLSCSDCL 120

Db 61 ASFRGLENCRCVDACKDRGDCWDFFEDTCVESTRIWMCNKFERGEBTRLEASLSCSDCL 120
 Qy 121 QRKDCCADYKSVCGQETTSWLBENCDTAQSQCPGEFDLPPVILFSMDGFRAEYLTYWDTL 180
 Db 121 QRKDCCADYKSVCGQETTSWLBENCDTAQSQCPGEFDLPPVILFSMDGFRAEYLTYWDTL 180
 Qy 181 MPNTNLKLTGCIHSKYMRAAMYPTKTFPNHYTIVGLYPESHGKGIDNNMMYDVNLINKNSLS 240
 Db 181 MPNTNLKLTGCIHSKYMRAAMYPTKTFPNHYTIVGLYPESHGKGIDNNMMYDVNLINKNSLS 240
 Qy 241 SKEQNPAWHQGPWKLTAMYQGLKAATFWPGSEVAANGSFPSIYMPYNGSPPFERIS 300
 Db 241 SKEQNPAWHQGPWKLTAMYQGLKAATFWPGSEVAANGSFPSIYMPYNGSPPFERIS 300
 Qy 301 TLKWLIDLPAERPRFTYMFPEEDSGHAGGPVSARTIKALQVVDHAFGMLMEGLIQRN 360
 Db 301 TLKWLIDLPAERPRFTYMFPEEDSGHAGGPVSARTIKALQVVDHAFGMLMEGLIQRN 360
 Qy 361 LHNCVNILLADHGMDQTVCNKNEMYMTDYPRFNFYMEGAPRRAHNIPHDFFSNS 420
 Db 361 LHNCVNILLADHGMDQTVCNKNEMYMTDYPRFNFYMEGAPRRAHNIPHDFFSNS 420
 Qy 421 BEIVNLSCKRPDKDHPKLPDPLPKRHYAKNVRIDKHLFQDQONLAVERKSNTICGG 480
 Db 421 BEIVNLSCKRPDKDHPKLPDPLPKRHYAKNVRIDKHLFQDQONLAVERKSNTICGG 480
 Qy 481 GHGYNNEFRSMEAIALFLAHPSPKEXTEVEPPENIEVNLMCDDLRQAPANGTHGSIN 540
 Db 481 GHGYNNEFRSMEAIALFLAHPSPKEXTEVEPPENIEVNLMCDDLRQAPANGTHGSIN 540
 Qy 541 HLLKVPFYEPSSHAEEVSFSVCGFANPLPTESDCPHQLNSTOLEVNOMNLNQEEI 600
 Db 541 HLLKVPFYEPSSHAEEVSFSVCGFANPLPTESDCPHQLNSTOLEVNOMNLNQEEI 600
 Qy 601 TATVKNLFGRRLVQGVNDLILIREYVSGFGRAMPMWSSTVPPQGDTSPLPPT 660
 Db 601 TATVKNLFGRRLVQGVNDLILIREYVSGFGRAMPMWSSTVPPQGDTSPLPPT 660
 Qy 661 VPDLRQDLYRVPSSEQKCSFPLADRNTHGFDPYPPASNRTSDQYDALITSNLVMYEE 720
 Db 661 VPDLRQDLYRVPSSEQKCSFPLADRNTHGFDPYPPASNRTSDQYDALITSNLVMYEE 720
 Qy 721 FRKWDYDPHSVLLKHAITERGNVWVSGPFDNYDGHFDADEITKHLANTDVPITHY 780
 Db 721 FRKWDYDPHSVLLKHAITERGNVWVSGPFDNYDGHFDADEITKHLANTDVPITHY 780
 Qy 781 FVVLTSCKNKSHTPENCEFGWLDJLPFLIPHRPTNVSCPEGKPEALWVEERFTAHTARVR 840
 Db 781 FVVLTSCKNKSHTPENCEFGWLDJLPFLIPHRPTNVSCPEGKPEALWVEERFTAHTARVR 840
 Qy 841 DYELLTGDFDYDKVQDVKYQPSVSEILQLKTYLPTPBTII 875
 Db 841 DYELLTGDFDYDKVQDVKYQPSVSEILQLKTYLPTPBTII 875

RESULT 9

US-10-291-241-16
 Sequence 16, Application US/10291241
 Publication No. US20030206905A1
 GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Faris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Pia M. Chaillita-Bid
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
 ; TITLE OF INVENTION: CANCER
 FILE REFERENCE: 51158-20062-20
 CURRENT APPLICATION NUMBER: 2003-10/291-241
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/005,480
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 10/062,109
 PRIOR FILING DATE: 2002-01-31
 PRIOR APPLICATION NUMBER: US 60/282,739
 NUMBER OF SEQ ID NOS: 103
 SEQ ID NO: 11
 LENGTH: 875
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-291-241-11

Query Match Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESTLTLATEOPVKNTLTKYKIACTVLLAVIMSLGLGLGLGRKLGKQGSRKKCFD 60
 Db 1 MESTLTLATEOPVKNTLTKYKIACTVLLAVIMSLGLGLGLGRKLGKQGSRKKCFD 60
 Qy 61 ASFRGLENCRCVDACKDRGDCWDFFEDTCVESTRIWMCNKFERGEBTRLEASLSCSDCL 120

CURRENT APPLICATION NUMBER:	US/10/291,241	
CURRENT FILING DATE:	2003-03-18	
PRIOR APPLICATION NUMBER:	US 10/005,480	
PRIOR FILING DATE:	2001-11-07	
PRIOR APPLICATION NUMBER:	US 10/062,109	
PRIOR FILING DATE:	2002-01-31	
PRIOR APPLICATION NUMBER:	US 60/282,739	
NUMBER OF SEQ ID NOS:	103	
SOFTWARE:	FastSEQ for Windows Version 4.0	
SEQ ID NO:	16	
LENGTH:	875	
TYPE:	PRT	
ORGANISM:	Homo Sapiens	
S-10-291-241-16		
Query Match	100.0%; Score 4804; DB 15; Length 875;	
Best Local Similarity	100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	
Matches	875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
y	1 MESTLTATQPVKNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60 1 MESTLTATQPVKNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60	
b	61 ASFRGLENCRDVCDVACKDRGDCCWIFEDCTVESTIWMCNKFRGETREASLCSCDCI 120 61 ASFRGLENCRDVCDVACKDRGDCCWIFEDCTVESTIWMCNKFRCEBTRLLASLCSDCL 120	
b	121 QKKDCCADYKSVQCGETSWLEENCDTAQQSCQPGFDLPPVILFSMDGFRAEYLTDTL 180 121 QKKDCCADYKSVQCGETSWLEENCDTAQQSCQPGFDLPPVILFSMDGFRAEYLTDTL 180	
b	121 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240 181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240	
b	181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240	
y	241 SKEQNPNPAWNGQPMWLAMYQGLKAATFWPGSEAVINGSFPSPYMPNGSYPPEEIS 300 241 SKEQNPNPAWNGQPMWLAMYQGLKAATFWPGSEAVINGSFPSPYMPNGSYPPEEIS 300	
b	301 TLLKWLDPKAERPRFYTMYFEEPDSSGHAGGPYSARVTKALQYDHAFGMLMEGLKORN 360	
b	301 TLLKWLDPKAERPRFYTMYFEEPDSSGHAGGPYSARVTKALQYDHAFGMLMEGLKORN 360	
y	361 LHNCYNIILLADHGMDQTYCNCMELYNTDYPRINFFYMEGAPRIRAINIPHDFFSNS 420 361 LHNCYNIILLADHGMDQTYCNCMELYNTDYPRINFFYMEGAPRIRAINIPHDFFSNS 420	
b	421 EETIVNLSCRPDQHFKPVLTPDLPKRLHAKNVRIDVHLFVDQQLAVRSKNTNCG 480 421 EETIVNLSCRPDQHFKPVLTPDLPKRLHAKNVRIDVHLFVDQQLAVRSKNTNCG 480	
y	481 GNHGTYNEFRNEATFLAHGSFSKBTETEVFENEVYNNMCDLIRIQAAPNNGTHGSIN 540 481 GNHGTYNEFRNEATFLAHGSFSKBTETEVFENEVYNNMCDLIRIQAAPNNGTHGSIN 540	
b	541 HLLKVPYEPSSHAEEYSKFSYCGFANPLPTESLDCFCPHIQNSTOLEQVNMLNTQEBI 600 541 HLLKVPYEPSSHAEEYSKFSYCGFANPLPTESLDCFCPHIQNSTOLEQVNMLNTQEBI 600	
b	601 TATVKYNUPEGRPRVLIQKNTDHCLYHREYSGFGKAMRMPMWSSYYTVPOLGDTSPPLPT 660 601 TATVKYNUPEGRPRVLIQKNTDHCLYHREYSGFGKAMRMPMWSSYYTVPOLGDTSPPLPT 660	
b	661 VPDCLRADYVAPPSESKCSFYLAQDNITHCFLYPPASNRTSQDYLALITSNLYPMYE 720 661 VPDCLRADYVAPPSESKCSFYLAQDNITHCFLYPPASNRTSQDYLALITSNLYPMYE 720	
b	721 FRKMDYFHSVLLKHTERENGVNVYSPIDPYNDGHDAPDEITKHLANTDPIPHY 780 721 FRKMDYFHSVLLKHTERENGVNVYSPIDPYNDGHDAPDEITKHLANTDPIPHY 780	
b	781 FVVLTSCKNSHTPENCWGMLDVLPLFPHRPTNYESPEGKPEALWEEFRTAIARVR 840	
Db	781 FVVLTSCKNSHTPENCWGMLDVLPLFPHRPTNYESPEGKPEALWEEFRTAIARVR 840	
Db	781 FVVLTSCKNSHTPENCWGMLDVLPLFPHRPTNYESPEGKPEALWEEFRTAIARVR 840	
Qy	841 DVELLTGGLDFQDKYQPVSBILQKTYLPLPFETTI 875	
Db	841 DVELLTGGLDFQDKYQPVSBILQKTYLPLPFETTI 875	
Db	RESULT 10 US-10-291-241-21 ; Sequence 21, Application US/102911241 ; Publication No. US2003020605A1	
	/ GENERAL INFORMATION: / APPLICANT: Agensys, Inc. / APPLICANT: Aya Jakobovits / APPLICANT: Arthur B. Raitano / APPLICANT: Mary Faris / APPLICANT: Rene S. Herbert / APPLICANT: Wangmiao Ge / APPLICANT: Karen Jane Meyrick Morrison / APPLICANT: Robert Kendall Morrison / APPLICANT: Pia M. Challie-Eid / TITLE OF INVENTION: NUCLEAR ACID AND CORRESPONDING PROTEIN / TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF / TITLE OF INVENTION: CANCER / FILE REFERENCE: 51158-20062_20 / CURRENT APPLICATION NUMBER: US/10/291,241 / CURRENT FILING DATE: 2003-03-18 / PRIOR APPLICATION NUMBER: US 10/005,480 / PRIOR FILING DATE: 2001-11-07 / PRIOR APPLICATION NUMBER: US 10/062,109 / PRIOR FILING DATE: 2002-01-31 / PRIOR APPLICATION NUMBER: US 60/282,739 / PRIOR FILING DATE: 2001-04-10 / NUMBER OF SEQ ID NOS: 103 / SOFTWARE: FastSEQ for Windows Version 4.0 / SEQ ID NO: 21 / LENGTH: 875 / TYPE: PRT / ORGANISM: Homo Sapiens US-10-291-241-21	
	Query Match	100.0%; Score 4804; DB 15; Length 875; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 MESTLTATQPVKNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60 1 MESTLTATQPVKNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60	1 MESTLTATQPVKNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60 1 MESTLTATQPVKNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60
	61 ASFRGLENCRDVCDVACKDRGDCCWIFEDCTVESTIWMCNKFRGETREASLCSCDCI 120 61 ASFRGLENCRDVCDVACKDRGDCCWIFEDCTVESTIWMCNKFRCEBTRLLASLCSDCL 120	1 MESTLTATEQPKVNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60 1 MESTLTATEQPKVNTLKKYKTAICIVILALLYIMSLGGGLRKLEKQGSCRKCFD 60
	121 QKKDCCADYKSVQCGETSWLEENCDTAQQSCQPGFDLPPVILFSMDGFRAEYLTDTL 180 121 QKKDCCADYKSVQCGETSWLEENCDTAQQSCQPGFDLPPVILFSMDGFRAEYLTDTL 180	61 ASFRGLENCRDVACDKDRGDCCWDFFDTCTVESTRIMCNKFRGEPLSCLCSDDCL 120 61 ASFRGLENCRDVACDKDRGDCCWDFFDTCTVESTRIMCNKFRGEPLSCLCSDDCL 120
	121 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240 181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240	61 ASFRGLENCRDVACDKDRGDCCWDFFDTCTVESTRIMCNKFRGEPLSCLCSDDCL 120 61 ASFRGLENCRDVACDKDRGDCCWDFFDTCTVESTRIMCNKFRGEPLSCLCSDDCL 120
	181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240	121 QKDCADCADYKSVQCGETSWLEENCDTAQQSCQPGFDLPPVILFSMDGFRAEYLTDTL 180 121 QKDCADCABYKSVQCGETSWLEENCDTAQQSCQPGFDLPPVILFSMDGFRAEYLTDTL 180
	241 SKEQNPNPAWNGQPMWLAMYQGLKAATFWPGSEAVINGSFPSPYMPNGSYPPEEIS 300 241 SKEQNPNPAWNGQPMWLAMYQGLKAATFWPGSEAVINGSFPSPYMPNGSYPPEEIS 300	121 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240 121 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240
	301 TLLKWLDPKAERPRFYTMYFEEPDSSGHAGGPYSARVTKALQYDHAFGMLMEGLKORN 360	181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240 181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240
	361 LHNCYNIILLADHGMDQTYCNCMELYNTDYPRINFFYMEGAPRIRAINIPHDFFSNS 420	181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240 181 MPNINKLKTGCGIHSKYMRAKYPTKTFPHNYTIVTGLYPSESHGILDNNMDVNLNKNSLS 240
	361 LHNCYNIILLADHGMDQTYCNCMELYNTDYPRINFFYMEGAPRIRAINIPHDFFSNS 420	241 SKEQNPNPAWNGQPMWLAMYQGLKAATFWPGSEAVINGSFPSPYMPNGSYPPEEIS 300 241 SKEQNPNPAWNGQPMWLAMYQGLKAATFWPGSEAVINGSFPSPYMPNGSYPPEEIS 300
	421 EETIVNLSCRPDQHFKPVLTPDLPKRLHAKNVRIDVHLFVDQQLAVRSKNTNCG 480	301 TLXKWLDPKAERPRFYTMYFEEPDSSGHAGGPVSARVTKALQYDHAFGMLMEGLKORN 360 301 TLXKWLDPKAERPRFYTMYFEEPDSSGHAGGPVSARVTKALQYDHAFGMLMEGLKORN 360
	421 EETIVNLSCRPDQHFKPVLTPDLPKRLHAKNVRIDVHLFVDQQLAVRSKNTNCG 480	361 LANCVNILLADHGMDOTYCNKMEYMTDYPRINFFYMEGAPRIRAHNIPHDFFFNS 420 361 LANCVNILLADHGMDOTYCNKMEYMTDYPRINFFYMEGAPRIRAHNIPHDFFFNS 420
	481 GNHGTYNEFRNEATFLAHGSFSKBTETEVFENEVYNNMCDLIRIQAAPNNGTHGSIN 540	361 LANCVNILLADHGMDQYCNMVEYMTDYPRINFFYMEGAPRIRAHNIPHDFFFNS 420 361 LANCVNILLADHGMDQYCNMVEYMTDYPRINFFYMEGAPRIRAHNIPHDFFFNS 420
	481 GNHGTYNEFRNEATFLAHGSFSKBTETEVFENEVYNNMCDLIRIQAAPNNGTHGSIN 540	

RESULT 11
US-10-291-241-22
Sequence 22, Application US/10291221
Publication No. US20030206905A1
GENERAL INFORMATION:
FILANT: Agensys, Inc.
APPLICANT: Aya Jakobovits
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Rene S. Hubert
APPLICANT: Wangmao Ge
APPLICANT: Karen Jane Meyrick Morrison
APPLICANT: Robert Kendall Morrison
APPLICANT: Pia M. Challita-Bid
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
TITLE OF INVENTION: CANCER
FILE REFERENCE: 51158-20062-20
CURRENT APPLICATION NUMBER: US/10/291,241
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 875
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-291-241-22

Qy 421 EEIYRNLSCKRPDOHFKPKYLTPDLPKRYHYAKNVRIDKWHLYDQWNLAVRSKSNTNGG 480
Db 421 EEIYRNLSCKRPDOHFKPKYLTPDLPKRYHYAKNVRIDKWHLYDQWNLAVRSKSNTNGG 480
Qy 481 GNHGYNNEERSMEAIFLAGPSFECEKTEVPPENIEVNLMCDLRLQAPAPNGTGSILN 540
Db 481 GNHGYNNEERSMEAIFLAGPSFECEKTEVPPENIEVNLMCDLRLQAPAPNGTGSILN 540
Qy 541 HLLKYPFPYRSHAREVSKESSVCGANPLTESLDCFCHLQNSTLQEVONQMLNLTQEII 600
Db 541 HLLKYPFPYRSHAREVSKESSVCGANPLTESLDCFCHLQNSTLQEVONQMLNLTQEII 600
Qy 601 TATVKVNLDFGRPRVYQKNDLKHREYVSGFGKAMRMNPWSSSYTVPOLGDTSPLPPT 660
Db 601 TATVKVNLDFGRPRVYQKNDLKHREYVSGFGKAMRMNPWSSSYTVPOLGDTSPLPPT 660
Qy 661 VPDCIRADRVPPSEQCSFYLAQDNTHGFLYPPASNRTSQQYDALITSNLVPMYE 720
Db 661 VPDCIRADRVPPSEQCSFYLAQDNTHGFLYPPASNRTSQQYDALITSNLVPMYE 720
Qy 721 FRKWDYFHSVLJLKHATRNGYNNVSGPFLFDNYDGHFADDEITKHLANTDVP1PHTY 780
Db 721 FRKWDYFHSVLJLKHATRNGYNNVSGPFLFDNYDGHFADDEITKHLANTDVP1PHTY 780
Qy 781 FVVLTSCKKSHTPENCPGWLDPFLPIHRPTNVESCPGKPEALWVEERTAHARVR 840
Db 781 FVVLTSCKKSHTPENCPGWLDPFLPIHRPTNVESCPGKPEALWVEERTAHARVR 840
Qy 841 DVELTGFLFYQKQVPSSEILQLKTLPTFETI 875
Db 841 DVELTGFLFYQKQVPSSEILQLKTLPTFETI 875

RESULT 12
US-10-291-241-81
Sequence 81, Application US/10291241
Publication No. US20030206905A1
GENERAL INFORMATION:
FILANT: Agensys, Inc.
APPLICANT: Aya Jakobovits
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Rene S. Hubert
APPLICANT: Wangmao Ge
APPLICANT: Karen Jane Meyrick Morrison
APPLICANT: Robert Kendall Morrison
APPLICANT: Pia M. Challita-Bid
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
TITLE OF INVENTION: CANCER
FILE REFERENCE: 51158-20062-20
CURRENT APPLICATION NUMBER: US/10/291,241
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 875
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-291-241-22

Qy 1 MESTIILATEQVKANTLKRYKIAIVILLIUMSGLGGLRURKGSCRKCFD 60
Db 1 MESTIILATEQVKANTLKRYKIAIVILLIUMSGLGGLRURKGSCRKCFD 60
Qy 61 ASFRGLIENCRCVDACKDRGDCWCDFEDTCYESTRWMCNKFRGCBTRLEASLSCSDCL 120
Db 61 ASFRGGIENCRCVDACKDRGDCWCDFEDTCYESTRWMCNKFRGCBTRLEASLSCSDCL 120
Qy 121 QKKDCCADYKSVCGQETSNLBENCDAQSOSQCPGFDLPPVILFSMDGFRAEYLTYWTDL 180
Db 121 QKRDCCADYKSVCGQETSNLBENCDAQSOSQCPGFDLPPVILFSMDGFRAEYLTYWTDL 180
Qy 181 MPNINKLKTGITHSKYMRAMYPTKTPNHTITVGLPESHGFTIDNNMYDVNLNKNTSLS 240
Db 181 MPNINKLKTGITHSKYMRAMYPTKTPNHTITVGLPESHGFTIDNNMYDVNLNKNTSLS 240
Qy 241 SKEQNINPAWHQGPWKMLTAMYQGLRAATFWPGSEVAINGSFPSIYMPYNGSYPFERRIS 300
Db 241 SKEQNINPAWHQGPWKMLTAMYQGLRAATFWPGSEVAINGSFPSIYMPYNGSYPFERRIS 300
Qy 361 LHNCVNLILADHOMDQTYCNKNEYMTYFPRINFNFYMEGPPAPRHAHNIPHDFFNS 420
Db 361 LHNCVNLILADHOMDQTYCNKNEYMTYFPRINFNFYMEGPPAPRHAHNIPHDFFNS 420
Qy 421 EETVNLSCRKPDQHFKPLTDPDKLRLHYAKNURIDKHLFQDQYKLAVRKSNTNCGG 480
Db 421 EETVNLSCRKPDQHFKPLTDPDKLRLHYAKNURIDKHLFQDQYKLAVRKSNTNCGG 480
Qy 481 GHGYNNEERSMEAIFLAGPSFKEKEVPPENIENYLNMDLRLTQAPANGTHGSILN 540
Db 481 GHGYNNEERSMEAIFLAGPSFKEKEVPPENIENYLNMDLRLTQAPANGTHGSILN 540
Qy 541 HLLKVPFYPSPHAEEVSKFSPVCCFANPLPTESDCFPHLQNSTLQEVONQMLNLTQEII 600
Db 541 HLLKVPFYPSPHAEEVSKFSPVCCFANPLPTESDCFPHLQNSTLQEVONQMLNLTQEII 600
Qy 601 TATVKVNLIPGPRPVLOKVNVDLCLLYREYVSGFGKAMRMPKWSSTYVQOLGDTSPLPPT 660
Db 601 TATVKVNLIPGPRPVLOKVNVDLCLLYREYVSGFGKAMRMPKWSSTYVQOLGDTSPLPPT 660
Qy 661 VPDCLRADYRVPPESEQCSKSFYLAQDNTHGFLYPPASNRTSQQYDALITSNLVPMYE 720
Db 661 VPDCLRADYRVPPESEQCSKSFYLAQDNTHGFLYPPASNRTSQQYDALITSNLVPMYE 720
Qy 721 FVVLTSCKKSHTPENCPGWLDPFLPIHRPTNVESCPGKPEALWVEERTAHARVR 840
Db 721 FVVLTSCKKSHTPENCPGWLDPFLPIHRPTNVESCPGKPEALWVEERTAHARVR 840
Qy 781 FVVLTSCKKSHTPENCPGWLDPFLPIHRPTNVESCPGKPEALWVEERTAHARVR 840
Db 781 FVVLTSCKKSHTPENCPGWLDPFLPIHRPTNVESCPGKPEALWVEERTAHARVR 840
Qy 841 DVBLLTGLDFYQDKVQPVSEILQLKTLPTFETI 875
Db 841 DVBLLTGLDFYQDKVQPVSEILQLKTLPTFETI 875

RESULT 12
US-10-291-241-81
Sequence 81, Application US/10291241
Publication No. US20030206905A1
GENERAL INFORMATION:
FILANT: Agensys, Inc.
APPLICANT: Aya Jakobovits
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Rene S. Hubert
APPLICANT: Wangmao Ge
APPLICANT: Karen Jane Meyrick Morrison
APPLICANT: Robert Kendall Morrison
APPLICANT: Pia M. Challita-Bid
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
TITLE OF INVENTION: CANCER
FILE REFERENCE: 51158-20062-20
CURRENT APPLICATION NUMBER: US/10/291,241
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 875
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-291-241-22

Qy 1 MESTIILATEQVKANTLKRYKIAIVILLIUMSGLGGLRURKGSCRKCFD 60
Db 1 MESTIILATEQVKANTLKRYKIAIVILLIUMSGLGGLRURKGSCRKCFD 60
Qy 100 0%; Score 4804; DB 15; Length 875;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Pia M. Challita-Eid
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
 CANCER

FILE REFERENCE: 51158-20062.20
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US/10/291-241
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US/10/005,480
 PRIOR FILING DATE: 2002-01-31
 PRIOR APPLICATION NUMBER: US/10/062,109
 PRIOR FILING DATE: 2002-07-30
 NUMBER OF SEQ ID NOS: 103
 SOFTWARE: FastSEQ For Windows Version 4.0
 SEQ ID NO: 81
 LENGTH: 875
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-291-241-81

Query Match Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 MESELTILATEQPYKNTLKKYKIACTIVLLVITYMSIGLGLGLRKEQGSCRKCFD 60
 Db 1 MESELTILATEQPYKNTLKKYKIACTIVLLVITYMSIGLGLGLRKEQGSCRKCFD 60
 Qy 61 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 Db 61 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 Qy 121 QKDCOCADAKYKSVCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 Db 121 QKDCOCADAKYKSVCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 Qy 181 MPNTNKLTKTGIAHKYMRAMYPIKTFPHYTTIVGLYFESHGIDDNMMYDNLNKNFLS 240
 Db 181 MPNTNKLTKTGIAHKYMRAMYPIKTFPHYTTIVGLYFESHGIDDNMMYDNLNKNFLS 240
 Qy 241 SKEQNPNPAWHGQPWMLTAMYQGLKAATYFWPGSEEVANGSFPSIYMYYNGSVPFEERIS 300
 Db 241 SKEQNPNPAWHGQPWMLTAMYQGLKAATYFWPGSEEVANGSFPSIYMYYNGSVPFEERIS 300
 Qy 301 TLKWLDPKAERPRFYTMYFEDPSGSCHAGGPYSARTIKALQVDFGMLMEGLKORN 360
 Db 301 TLKWLDPKAERPRFYTMYFEDPSGSCHAGGPYSARTIKALQVDFGMLMEGLKORN 360
 Qy 361 LHCNCYNIIILADHGMDCTYCNKVEYMTDFPRINFYMYEGPAPRIRHNIPHDFFSNS 420
 Db 361 LHCNCYNIIILADHGMDCTYCNKVEYMTDFPRINFYMYEGPAPRIRHNIPHDFFSNS 420
 Qy 421 EETVNLSCKRKPDQHPKPYLTPLDKRHYAKVTRIDYVHLFDQONLAVRKSNTNCGG 480
 Db 421 EETVNLSCKRKPDQHPKPYLTPLDKRHYAKVTRIDYVHLFDQONLAVRKSNTNCGG 480
 Qy 481 GNHGTYNNEPFSMEAFLAHGSPSFEKTEYEPFENIEVNLCDLRLQAPANGTHSSLN 540
 Db 481 GNHGTYNNEPFSMEAFLAHGSPSFEKTEYEPFENIEVNLCDLRLQAPANGTHSSLN 540
 Qy 541 HLLKVPFYEPSHAEEVKSFVCGFANPLPTESLDCFCPHLQNSTOLEQYQNMNLTOEBI 600
 Db 541 HLLKVPFYEPSHAEEVKSFVCGFANPLPTESLDCFCPHLQNSTOLEQYQNMNLTOEBI 600
 Qy 601 TATVKVNLPGGRPRVYQKNDVHCLLYHREYVSFGFKAMEMPMASSTYVQLGDTSPPLPT 660
 Db 601 TATVKVNLPGGRPRVYQKNDVHCLLYHREYVSFGFKAMEMPMASSTYVQLGDTSPPLPT 660
 Qy 661 VPDCLRADYRVPPSSQKCSFYLADKNITHGFLYPPASNRTSQDYALITSNLVPKYEE 720
 Db 661 VPDCLRADYRVPPSSQKCSFYLADKNITHGFLYPPASNRTSQDYALITSNLVPKYEE 720
 Qy 721 FRKMDYFHSVLLJKHATERGVNVVSGPFDYNYDGHFDAPDEBKHLANTDVPPIPHY 780
 Db 721 FRKMDYFHSVLLJKHATERGVNVVSGPFDYNYDGHFDAPDEBKHLANTDVPPIPHY 780
 Qy 781 FVVLTSCKNKSHTPNCPCGMWLDVLPFLPHRPTVNESCPEGKDEALWVEERFTAHIAVR 840
 Db 781 FVVLTSCKNKSHTPNCPCGMWLDVLPFLPHRPTVNESCPEGKDEALWVEERFTAHIAVR 840
 Qy 841 DVELLIGLDFYQDKYQPSSEILQLKTYLPTFETI 875
 Db 841 DVELLIGLDFYQDKYQPSSEILQLKTYLPTFETI 875

RESULT 13
 US-10-291-241-94
 ; Sequence 94, Application US/10291241
 ; Publication No. US20030206305A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Mary Paris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Merrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Pia M. Challita-Eid
 ; TITLE OF INVENTION: NUCLEAR ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 51158-20062-20
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 10/062,109
 ; PRIOR FILING DATE: 2002-07-30
 ; NUMBER OF SEQ ID NOS: 103
 ; SBQ ID: NO 94
 ; LENGTH: 875
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-291-241-94

Query Match 100.0%; Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 MESELTILATEQPYKNTLKKYKIACTIVLLVITYMSIGLGLGLRKEQGSCRKCFD 60
 Db 1 MESELTILATEQPYKNTLKKYKIACTIVLLVITYMSIGLGLGLRKEQGSCRKCFD 60
 Qy 61 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 Db 61 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 Qy 121 QKDCOCADAKYKSVCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 Db 121 QKDCOCADAKYKSVCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 Qy 181 MPNTNKLTKTGIAHKYMRAMYPIKTFPHYTTIVGLYFESHGIDDNMMYDNLNKNFLS 240
 Db 181 MPNTNKLTKTGIAHKYMRAMYPIKTFPHYTTIVGLYFESHGIDDNMMYDNLNKNFLS 240
 Qy 241 SKEQNPNPAWHGQPWMLTAMYQGLKAATYFWPGSEEVANGSFPSIYMYYNGSVPFEERIS 300
 Db 241 SKEQNPNPAWHGQPWMLTAMYQGLKAATYFWPGSEEVANGSFPSIYMYYNGSVPFEERIS 300
 Qy 301 TLKWLDPKAERPRFYTMYFEDPSGSCHAGGPYSARTIKALQVDFGMLMEGLKORN 360
 Db 301 TLKWLDPKAERPRFYTMYFEDPSGSCHAGGPYSARTIKALQVDFGMLMEGLKORN 360
 Qy 361 LHCNCYNIIILADHGMDCTYCNKVEYMTDFPRINFYMYEGPAPRIRHNIPHDFFSNS 420
 Db 361 LHCNCYNIIILADHGMDCTYCNKVEYMTDFPRINFYMYEGPAPRIRHNIPHDFFSNS 420
 Qy 421 EETVNLSCKRKPDQHPKPYLTPLDKRHYAKVTRIDYVHLFDQONLAVRKSNTNCGG 480
 Db 421 EETVNLSCKRKPDQHPKPYLTPLDKRHYAKVTRIDYVHLFDQONLAVRKSNTNCGG 480
 Qy 481 GNHGTYNNEPFSMEAFLAHGSPSFEKTEYEPFENIEVNLCDLRLQAPANGTHSSLN 540
 Db 481 GNHGTYNNEPFSMEAFLAHGSPSFEKTEYEPFENIEVNLCDLRLQAPANGTHSSLN 540
 Qy 541 HLLKVPFYEPSHAEEVKSFVCGFANPLPTESLDCFCPHLQNSTOLEQYQNMNLTOEBI 600
 Db 541 HLLKVPFYEPSHAEEVKSFVCGFANPLPTESLDCFCPHLQNSTOLEQYQNMNLTOEBI 600
 Qy 601 TATVKVNLPGGRPRVYQKNDVHCLLYHREYVSFGFKAMEMPMASSTYVQLGDTSPPLPT 660
 Db 601 TATVKVNLPGGRPRVYQKNDVHCLLYHREYVSFGFKAMEMPMASSTYVQLGDTSPPLPT 660
 Qy 661 VPDCLRADYRVPPSSQKCSFYLADKNITHGFLYPPASNRTSQDYALITSNLVPKYEE 720
 Db 661 VPDCLRADYRVPPSSQKCSFYLADKNITHGFLYPPASNRTSQDYALITSNLVPKYEE 720
 Qy 721 FRKMDYFHSVLLJKHATERGVNVVSGPFDYNYDGHFDAPDEBKHLANTDVPPIPHY 780
 Db 721 FRKMDYFHSVLLJKHATERGVNVVSGPFDYNYDGHFDAPDEBKHLANTDVPPIPHY 780
 Qy 781 FVVLTSCKNKSHTPNCPCGMWLDVLPFLPHRPTVNESCPEGKDEALWVEERFTAHIAVR 840
 Db 781 FVVLTSCKNKSHTPNCPCGMWLDVLPFLPHRPTVNESCPEGKDEALWVEERFTAHIAVR 840
 Qy 841 DVELLIGLDFYQDKYQPSSEILQLKTYLPTFETI 875
 Db 841 DVELLIGLDFYQDKYQPSSEILQLKTYLPTFETI 875

1 MESELTILATEQPYKNTLKKYKIACTIVLLVITYMSIGLGLGLRKEQGSCRKCFD 60
 1 MESELTILATEQPYKNTLKKYKIACTIVLLVITYMSIGLGLGLRKEQGSCRKCFD 60
 1 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 1 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 1 QKDCOCADAKYKSVCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 1 QKDCOCADAKYKSVCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 1 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 1 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 1 QKDCOCADYKSYCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 1 QKDCOCADYKSYCOGETSMILEENCDTAQOSQCPCBGFDLPPVILFSMDGFRAYLYTWTDL 180
 1 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 1 ASFRGLENCRDYACKDRGDCWDFFDTCCESTRIMNKFRGETREASLCSDDCL 120
 1 MPNTNKLTKTGIAHKYMRAMYPIKTFPHYTTIVGLYFESHGIDDNMMYDNLNKNFLS 240
 1 MPNTNKLTKTGIAHKYMRAMYPIKTFPHYTTIVGLYFESHGIDDNMMYDNLNKNFLS 240
 1 SKEQNPNPAWHGQPWMLTAMYQGLKAATYFWPGSEEVANGSFPSIYMYYNGSVPPEERIS 300
 1 SKEQNPNPAWHGQPWMLTAMYQGLKAATYFWPGSEEVANGSFPSIYMYYNGSVPPEERIS 300
 1 TLLKWLDPKAERPRFYTMYFEDPSGSCHAGGPYSARTIKALQVDFGMLMEGLKORN 360
 1 TLLKWLDPKAERPRFYTMYFEDPSGSCHAGGPYSARTIKALQVDFGMLMEGLKORN 360

RESULT 14
 US-10-291-241-95
 ; Sequence 95, Application US/10291241
 ; Publication No. US20030206905A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Faris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Pia M. Challita-Bid
 ; TITLE OF INVENTION: NUCLIC ACID AND CORRESPONDING PROTEIN
 ; FILE REFERENCE: 51158-20062-20
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 10/062,109
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/282,739
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: Fastaseq For Windows Version 4.0
 ; SEQ ID NO: 95
 ; LENGTH: 875
 ; TYPE: PR
 ; ORGANISM: Homo Sapiens
 ; US-10-291-241-95

Db 301 TLKWLDPKAERPRFTYMYFEEPDSSGHAGGPVSARYVKALQVDAFAFGMLMEGLKORN 360
 Db 361 LHNCVNIIILLADHGMDOTCNKNEYMTDFPRINFYMEGAPAPIRHNIPHDFFSFNS 420
 Qy 361 LHNCVNIIILLADHGMDOTCNKNEYMTDFPRINFYMEGAPAPIRHNIPHDFFSFNS 420
 Db 422 EETVRNLSCKRPDKDHFKPYLTDPDKRLHYAKNRVIDKVLFLFDQQLAVRSKSNTNCGG 480
 Qy 422 EETVRNLSCKRPDKDHFKPYLTDPDKRLHYAKNRVIDKVLFLFDQQLAVRSKSNTNCGG 480
 Qy 481 GHGYNNEFRSMEAIFIAGPSFEKEKTEVEPPENIEYNIMCDLIRIOPAPNGTHGSILN 540
 Db 481 GHGYNNEFRSMEAIFIAGPSFEKEKTEVEPPENIEYNIMCDLIRIOPAPNGTHGSILN 540
 Qy 541 HLLKVPFPYPSHAEVSKSVCPANPLPTESDLCPHLQNOSTQEONQMLNLTQEET 600
 Db 541 HLLKVPFPYPSHAEVSKSVCPANPLPTESDLCPHLQNOSTQEONQMLNLTQEET 600
 Qy 601 TATVKVNLFPGRPVQLQNVDHCLYHREYVSGFKAMRMPPMSSTVQLGDTSPLPPT 660
 Db 601 TATVKVNLFPGRPVQLQNVDHCLYHREYVSGFKAMRMPPMSSTVQLGDTSPLPPT 660
 Qy 661 VPDCLRADRVPPSEQSQCSFLAYDKNITHGTYPPASNRTSDQXDALITSNLVMEYE 720
 Db 661 VPDCLRADRVPPSEQSQCSFLAYDKNITHGTYPPASNRTSDQXDALITSNLVMEYE 720
 Qy 722 FRKWDYFFSVLJLKHTERTRGYNVVSQPIFDYNYDGHDADEITKHLANTDVP1PHTY 780
 Db 722 FRKWDYFFSVLJLKHTERTRGYNVVSQPIFDYNYDGHDADEITKHLANTDVP1PHTY 780
 Qy 781 FVVLTSCKNKSHPENCQWLDVLPF1IPHRPTNVSCPEKGPEALWVERFTAHARVR 840
 Db 781 FVVLTSCKNKSHPENCQWLDVLPF1IPHRPTNVSCPEKGPEALWVERFTAHARVR 840
 Qy 841 DVELLTGLDFYQDKVQPVSEIOLKVLPTFETTI 875
 Db 841 DVELLTGLDFYQDKVQPVSEIOLKVLPTFETTI 875
 Query Match 100.0%; Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MESTLTLATEBQPVKRNTRKVKIACTIVLLALIIMSGLGLGLGLKLEKGSSCRKCFD 60
 Db 1 MESTLTLATEBQPVKRNTRKVKIACTIVLLALIIMSGLGLGLGLKLEKGSSCRKCFD 60
 Qy 61 ASFRGLENCECDVACKDRGDCCNDFEDTCVESTRWMCNKFRGETRLEASLCSDDCL 120
 Db 61 ASFRGLENCECDVACKDRGDCCNDFEDTCVESTRWMCNKFRGETRLEASLCSDDCL 120
 Qy 121 QKKDCADYKSVCOGETSWLBEENCDTAQOQSQCPEGFDLPPVILFSMDGFRAEYLTVTDL 180
 Db 121 QKKDCADYKSVCOGETSWLBEENCDTAQOQSQCPEGFDLPPVILFSMDGFRAEYLTVTDL 180
 Qy 181 MPNTNKLKTCGIRSKYMRAMYPTKTPHNTYITVGLYPBSHGIGIDNNNNYDVNLNKFLSL 240
 Db 181 MPNTNKLKTCGIRSKYMRAMYPTKTPHNTYITVGLYPBSHGIGIDNNNNYDVNLNKFLSL 240
 Qy 241 SKEQNNPWVHGPQPMWLTAMYQGKATAFWPSEVAENGSPSISYMPYNGSYPFEPBIS 300
 Db 241 SKEQNNPWVHGPQPMWLTAMYQGKATAFWPSEVAENGSPSISYMPYNGSYPFEPBIS 300
 Qy 301 TLLKWLDPKAERPRFTYMFEEPDSSGHAGGPVSARYVKALQVDAFAFGMLMEGLKORN 360
 Db 301 TLLKWLDPKAERPRFTYMFEEPDSSGHAGGPVSARYVKALQVDAFAFGMLMEGLKORN 360
 Qy 361 LHNCVNIIILLADHGMDOTCNKNEYMTDFPRINFYMEGAPAPIRHNIPHDFFSFNS 420
 Db 361 LHNCVNIIILLADHGMDOTCNKNEYMTDFPRINFYMEGAPAPIRHNIPHDFFSFNS 420
 Qy 421 EEIVRNLSCKRPDKDHFKPYLTDPDKRLHYAKNRVIDKVLFLFDQQLAVRSKSNTNCGG 480
 Db 421 EEIVRNLSCKRPDKDHFKPYLTDPDKRLHYAKNRVIDKVLFLFDQQLAVRSKSNTNCGG 480
 Qy 481 GHGYNNEFRSMEAIFIAGPSFEKEKTEVEPPENIEYNIMCDLIRIOPAPNGTHGSILN 540
 Db 481 GHGYNNEFRSMEAIFIAGPSFEKEKTEVEPPENIEYNIMCDLIRIOPAPNGTHGSILN 540
 Qy 541 HLLKVPFPYPSHAEVSKSVCPANPLPTESDLCPHLQNOSTQEONQMLNLTQEET 600
 Db 541 HLLKVPFPYPSHAEVSKSVCPANPLPTESDLCPHLQNOSTQEONQMLNLTQEET 600
 Qy 601 TATVKVNLFGRPRVQLQNVDHCLYHREYVSGFKAMRMPPMSSTVQLGDTSP1PPT 660
 Db 601 TATVKVNLFGRPRVQLQNVDHCLYHREYVSGFKAMRMPPMSSTVQLGDTSP1PPT 660
 Qy 661 VPDCLRADRVPPSEQSQCSFLAYDKNITHGTYPPASNRTSDQXDALITSNLVMEYE 720
 Db 661 VPDCLRADRVPPSEQSQCSFLAYDKNITHGTYPPASNRTSDQXDALITSNLVMEYE 720
 Qy 722 FRKWDYFFSVLJLKHTERTRGYNVVSQPIFDYNYDGHDADEITKHLANTDVP1PHTY 780
 Db 722 FRKWDYFFSVLJLKHTERTRGYNVVSQPIFDYNYDGHDADEITKHLANTDVP1PHTY 780
 Qy 781 FVVLTSCKNKSHPENCQWLDVLPF1IPHRPTNVSCPEKGPEALWVERFTAHARVR 840
 Db 781 FVVLTSCKNKSHPENCQWLDVLPF1IPHRPTNVSCPEKGPEALWVERFTAHARVR 840
 Qy 841 DVELLTGLDFYQDKVQPVSEIOLKVLPTFETTI 875
 Db 841 DVELLTGLDFYQDKVQPVSEIOLKVLPTFETTI 875
 RESULT 15
 US-10-231-241-96
 ; Sequence 96, Application US/10291241
 ; Publication No. US20030206905A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Faris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Pia M. Challita-Bid
 ; TITLE OF INVENTION: NUCLIC ACID AND CORRESPONDING PROTEIN
 ; FILE REFERENCE: 51158-20062-20
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 10/062,109
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/282,739
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: Fastaseq For Windows Version 4.0
 ; SEQ ID NO: 95
 ; LENGTH: 875
 ; TYPE: PR
 ; ORGANISM: Homo Sapiens
 ; US-10-291-241-95

; Sequence 96, Application US/10291241
 ; Publication No. US20030206905A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano

APPLICANT: Mary Paris
 i APPLICANT: Rene S. Hubert
 i APPLICANT: Wangmao Ge
 i APPLICANT: Karen Jane Meyrick Morrison
 i APPLICANT: Robert Kendall Morrison
 i APPLICANT: Pia M. Chalica-Eid
 i TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 i TITLE OF INVENTION: ENTITLED 161PZF10B USEFUL IN TREATMENT AND DETECTION OF
 i TITLE OF INVENTION: CANCER
 i CURRENT APPLICATION NUMBER: US/10/291,241
 i CURRENT FILING DATE: 2003-03-18
 i PRIOR APPLICATION NUMBER: US 10/005,480
 i PRIOR FILING DATE: 2001-11-07
 i PRIOR APPLICATION NUMBER: US 10/062,109
 i PRIOR FILING DATE: 2002-01-31
 i PRIOR APPLICATION NUMBER: US 10/282,739
 i PRIOR FILING DATE: 2001-04-10
 i NUMBER OF SEQ ID NOS: 103
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 96
 i LENGTH: 875
 i TYPE: PRT
 i ORGANISM: Homo Sapiens
 US-10-291-241-96

Query Match 100.0%; Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 875; Conservative 0;

Qy	Db	Score	Length
1 MESTLTLATEOPVKONTLKEYKIACTVLLAVIMSLGLGLGLGLRKLKEQGSCRKCFD	1 MESTLTLATEOPVKONTLKEYKIACTVLLAVIMSLGLGLGLGLRKLKEQGSCRKCFD	60	60
61 ASFRGLENCRCDVACKDRGDCCWDFFDTCVBSTRIWMCNKFRCGETRLASLGSCSDCI	61 ASFRGLENCRCDVACKDRGDCCWDFFDTCVBSTRIWMCNKFRCGETRLASLGSCSDCI	120	120
121 QKKDCCADYKSVQCGETSWLEBENCDAQQSOCPEGFDLPPVILFSMDGFRAEYLWTDTL	121 QKDCCADYKSVQCGETSWLEBENCDAQQSOCPEGFDLPPVILFSMDGFRAEYLWTDTL	180	180
181 MPNNINKLKTCGTHSKYMRAMYPTKTFPHNTIVTGLYPESHGTDNNYDVNLNKNSLS	181 MPNNINKLKTCGTHSKYMRAMYPTKTFPHNTIVTGLYPESHGTDNNYDVNLNKNSLS	240	240
241 SKEQNMPAHHQGPMLTANQHQLKATAYFMPGSEVAINTSFPSYMPNGSYVPEERTIS	241 SKEQNMPAHHQGPMLTANQHQLKATAYFMPGSEVAINTSFPSYMPNGSYVPEERTIS	300	300
301 TLWKWLDPKAERPRFTMYFEPDSSGHAGGPSARVITALQYDHAEGMLMEGLKQRN	301 TLWKWLDPKAERPRFTMYFEPDSSGHAGGPSARVITALQYDHAEGMLMEGLKQRN	360	360
361 LHNCVNILLADHGMDTCKNMEINTDFPRINFYMMEGPAPRARNIPHDFFSNS	361 LHNCVNILLADHGMDTCKNMEINTDFPRINFYMMEGPAPRARNIPHDFFSNS	420	420
421 ERIVRNLSCKRDQHFKPYLPDLPEKRLHYAKNRIDKVHLFDQDWLAVRSKSNTNCGG	421 ERIVRNLSCKRDQHFKPYLPDLPEKRLHYAKNRIDKVHLFDQDWLAVRSKSNTNCGG	480	480
481 GNHGYNNEFRSMEAIFIAGHGPSFKEKEVEPFENTEVYNLMCDLIRIOPAPNNGTHGSLN	481 GNHGYNNEFRSMEAIFIAGHGPSFKEKEVEPFENTEVYNLMCDLIRIOPAPNNGTHGSLN	540	540
541 HLLKVPYEPSPHAEVYKESVGFANPLPTSLDCHPQLONSTQEYQNMNLTOEEI	541 HLLKVPYEPSPHAEVYKESVGFANPLPTSLDCHPQLONSTQEYQNMNLTOEEI	600	600
601 TATVKVN-LPGSPRVLQKNDVHCLLYREYVSGFGKAMRMNWSSYTVPQLGDTESPLPPT	601 TATVKVN-LPGSPRVLQKNDVHCLLYREYVSGFGKAMRMNWSSYTVPQLGDTESPLPPT	660	660
661 VPDCILRADVYPPSESOKCSFYLAQKNITHGFLYPPASNRTSDSOYDALITSNLYPMYEE	661 VPDCILRADVYPPSESOKCSFYLAQKNITHGFLYPPASNRTSDSOYDALITSNLYPMYEE	720	720
661 VPDCILRADVYPPSESOKCSFYLAQKNITHGFLYPPASNRTSDSOYDALITSNLYPMYEE	661 VPDCILRADVYPPSESOKCSFYLAQKNITHGFLYPPASNRTSDSOYDALITSNLYPMYEE	720	720
721 FRKMDYFHSQLLKHATERGVNVYSGP1FDNYDGHFDAPDETKHLANTDVF1PHTY	721 FRKMDYFHSQLLKHATERGVNVYSGP1FDNYDGHFDAPDETKHLANTDVF1PHTY	780	780
721 FRKMDYFHSQLLKHATERGVNVYSGP1FDNYDGHFDAPDETKHLANTDVF1PHTY	721 FRKMDYFHSQLLKHATERGVNVYSGP1FDNYDGHFDAPDETKHLANTDVF1PHTY	780	780
781 FVVLTSCKNSHTPENCPGMIDVLPFI1PHRPTNYESCPBKPEALWVEERFTAHARVR	781 FVVLTSCKNSHTPENCPGMIDVLPFI1PHRPTNYESCPBKPEALWVEERFTAHARVR	840	840
781 FVVLTSCKNSHTPENCPGMIDVLPFI1PHRPTNYESCPBKPEALWVEERFTAHARVR	781 FVVLTSCKNSHTPENCPGMIDVLPFI1PHRPTNYESCPBKPEALWVEERFTAHARVR	840	840
841 DVELLTGGLDFYODKQVOPVSEIOLQKTYLPFTETTI	841 DVELLTGGLDFYODKQVOPVSEIOLQKTYLPFTETTI	875	875
841 DVELLTGGLDFYODKQVOPVSEIOLQKTYLPFTETTI	841 DVELLTGGLDFYODKQVOPVSEIOLQKTYLPFTETTI	875	875

Search completed: July 6, 2004, 13:26:07
 Job time : 59 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:11:52 ; Search time 26 Seconds
(without alignments)

3237.215 Million cell updates/sec

Title: US-10-005-480A-743

Perfect score: 1 METIILTATEQPYFKNTLKK.....QPVSEILQLKTYLPFETTI 875

Sequence: Gapop 10.0 , Gapext 0.5

Scoring table: BLOSSOM62

hypothetical prote

phosphonoacetate h

tubulointerstitial

placental protein

probable membrane

alpha-2-macroglobu

hypothetical prote

integrin beta3 - C

hypothetical prote

major facilitator

storage protein 2

hypothetical prote

glucocorticoid-sen

hypothetical prote

guanidine nucleoti

ALIGNMENTS

Total number of hits satisfying chosen parameters: 283366

RESULT 1
A57080
cell surface antigen RB13-6 - rat
N;Contains: phosphodiesterase I (EC 3.1.4.1)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: A57080
R;Deisler, H.; Loeffelholz, P.; Rajewsky, M.F.
J. Biol. Chem. 270, 9849-9855, 1995
A;Title: Affinity purification and cDNA cloning of rat neural differentiation and tumor
A;Reference number: A57080; MUID:9524775; PMID:730366
A;Accession: A57080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-855 <DEBI>
A;Cross-references: GB:247987; NID:9806378; PID:CAA88029.1; PID:9806379
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase; su-

F;1-22/Domain: cytosolic #status Predicted <CYT>
F;23-45/Domain: transmembrane #status Predicted <TMN>
F;46-975/Domain: extracellular #status Predicted <EXT>
F;51-94/Domain: somatomedin B homology <SBG>
F;95-138/Domain: somatomedin B homology <SBH2>

F;237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status P,
P;237,280,289,533,574,594,702,789/Binding site: carbohydride (Asn) (covalent) #status P,

Query Match 82.1%; Score 3972; DB 1; Length 875;
Best Local Similarity 81.2%; Pred. No. 7.2e-272;
Matches 711; Conservative 77; Mismatches 86; Indels 2; Gaps 2;

1 MESTIILATEQPVKNTLKKYKACIVILLYMSLGGLGLRKLEKQ-GSCKRKCF 59
Qy :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
1 MDSRLALATEPIKMDSLKRYKILQALLLMLVSLGLGLGLRPEEHGSCKRKCF 60

60 DASFRGLENCRCDVAKCKDREDCCMDFEDTCVESTRMNCNKFRGCTRLEASLCSDDC 119
Qy :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
61 DSSHRLIEGRCDSSCTDRGCDMDFEDTCVKSQIWTNSFRGCTRLEALCSADD 120

60 LQKKKCCADYKSVCGCGETSWLBNENQDTAQSQCPBEGFDLPPVILSMGFRAEYLWDT 179
Qy :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
121 LQRKQCCDTDKAVCQGEVPNVAEASSOBPQCPEGFDQPPVILSMGFRAEYLQWST 180

180 IMPNNINKLKKGIGIHKYMEAMYPKTFPHYTIVGLXPESHGIDINNNMYDYNLNQFSL 239
Qy :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
181 LLPNNINKLKKGIGIHKYMEAMYPKTFPHYTIVGLXPESHGIDINNNMYDYNLNQFSL 240

240 SSKEQNNPAWFGQPMWLTAMYQGLKAATYFMPDSEVAINGSPSPIMYPNGSVPFERI 299
Qy :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:
241 SSVEKSNPAWWSQQIWLTAMYQGLKAASYWIGLSDVANGSPNITRNYSNSVPEESRI 300

300 STLLKWDLPLKAERRPRFTVNYFPEPDSSSHAGGPVSARVIAKQVVDHARGMLMEGXQR 359
Qy :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
29

Searched: 283366 seqs, 96191526 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39/2	82.7	875	A57080	cell surface antigen
2	2498.5	52.0	925	1 A39216	nucleotide diphosp
3	2411.5	50.2	905	1 A27410	nucleotide diphosp
4	2043.5	42.5	885	1 A55453	nucleotide diphosp
5	2040.5	42.5	915	1 A55144	autotaxin precursor
6	743.5	15.5	496	2 T09931	probable phosphodi
7	737.5	15.4	479	2 T03293	probable phosphodi
8	712.5	14.8	457	2 T09932	probable phosphodi
9	680.5	14.2	461	2 T09933	probable phosphodi
10	644.0	13.4	477	1 A59390	probable phosphodi
11	637.0	13.3	485	2 T40657	probable phosphodi
12	632.5	13.2	477	1 A59391	probable phosphodi
13	632.0	13.2	300	2 A41179	protein kinase PC
14	630.5	13.1	429	2 T33724	probable phosphodi
15	629.5	13.1	453	1 A59389	probable phosphodi
16	623.0	13.0	829	2 T19494	hypothetical prote
17	553.0	11.5	451	2 F87407	probable phosphodi
18	508.0	10.6	674	2 T19495	hypothetical prote
19	499.5	10.4	433	2 B2537	probable phosphodi
20	434.0	9.0	743	2 S19437	hypothetical prote
21	412.5	8.6	493	2 S55443	probable phosphodi
22	374.0	7.8	614	2 T03093	hypothetical prote
23	301.0	6.3	96	2 A25274	phosphodiesterase
24	222.5	4.6	434	2 F86958	AP superfamily [im
25	222.5	4.6	453	2 T16795	hypothetical prote
26	212.0	4.4	133	2 T09934	hypothetical prote
27	209.0	4.4	422	2 A51252	pyrophosphatase ho
28	195.5	4.1	422	2 AH1614	weakly Pyrophospho
29	150.0	3.1	360	2 T20867	hypothetical prote

Db	301	ATLQWDLPKAERPSFYTIVVEPPDSAGIKSGPVSAVTKALQLVDDAFGMLMEGLKQR	360	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-80 <BEI>
Qy	360	NLHNCVNLIILADHGMDQTYCNKMYMTDFPRINFEYNYGCPAPRIBAHNTIHDFFPSEN	419	C; Genetics: C; Species: Homo sapiens (man) C; Accession: GB:J05654 C; Status: it is uncertain whether Met-1 or Met-53 is the initiator
Db	361	NLHNCVNLIILADHGMDQTSRDRVXMTDFPEIN-FYNYGCPAPRIRTRNPQDFETEN	419	C; Cross-references: GB:J05654 C; Molecule type: mRNA C; Residues: 1-325 <UNL1> C; Accession: S23587 C; Status: not compared with conceptual translation
Db	420	SEBIVRNLSCRKPDKPFKPLTDPKPLHYAKNVRIDKVLHFDQNLAVRSKSNTNCG	479	C; Superfamily: nucleotide pyrophosphatase / somatomedin B homology C; Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphotriester hydrolase; transmembrane domain; predicted E:77-97 Domain: transmembrane 4 status Predicted F:104-144 Domain: somatomedin B homology <SBH1> F:145-188 Domain: somatomedin B homology <SBH2> F:179-285,341-477,578-585,643-700,731-748 Binding site: carbohydrate (Asn) (covalent) #status predicted F:256/Binding site: AMP (Thr) (covalent) #status predicted
Qy	420	SEBIVRNLSCRKPDKPFKPLTDPKPLHYAKNVRIDKVLHFDQNLAVRSKSNTNCG	479	Query Match Score 2498.5; DB 1; Length 925; Best Local Similarity 53.1%; Pred. No. 6e-1695 Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;
Db	480	GGMHGYNNEFRSMEAIPLAIGPSFKEKTYEPFENIEVNLMCDLIRIOPADNGTHGSL	539	Qy 10 EQPVRK ---NTLK---KYKIACTIVLALLYIMSLGFLGLRKLEKGOSCRKKCFDAS 62 Db 57 EEPLEKAARPARTAKDPTYRVSILVYPCAKVPSCKGRCPERT 116
Qy	480	GGETHGZNNEFKSMEAIPLAIGPSFKEKTYEPFENIEVNLMCDLIRIOPADNGTHGSL	539	Qy 63 FRLGLENCRCVDACKDRCGCCWDFDTCTVESTRIMMWNKFRGCTRELASICCSCDCLQK 122 Db 117 F---GNCRDAACVELGNQCLDQYQETCIEPHIWTCNKFRGCKELTRSACSDCDRK 173
Qy	540	NELLKRPFYEPSEHABEVSKPSVCGFANPLPTESDLFCFHQNLSLQLEQVNQMLNLTQE	599	Qy 123 KDCGADYKSVCOGETSNIEENDTAQQSQOCBEGFDLPVULFMSMDGRARYLYWTDTIMP 182 Db 720 EFKRMWDYFHSSVLKHTGATERBNGVNVSPGIFDYNYGHFDADEBITHLANTDVP1PTH 779 Db 720 EFKRMWDYFHSSVLKHTGATERBNGVNVSPGIFDYNYGHFDAPEITINVAGTDVPTPH 779 Db 174 GDCCUNYSSVCQEBKSYVEPCESINPQCPAGEFPPTPLFSLDGFRAYLHTWGLLLP 233
Db	600	VSATEKTNLPLPGRPRVTLQKNDKDHCLLYREYVSGFKAMKMPKNSYTVPKGDTSLLP	659	Qy 183 NINKLTGIGHSKYMRAAMYPTKTPHNTYITVGLYBPSKGITIDNNMMYDYNLNKNPSSLSSK 242 Db 234 VISKLKCCOTYQMRPVYPTKTFPHNTYITVGLYBPSKGITIDNNMMYDYNLNKNPSSLSSK 293 Db 243 EONNPWAHHQGPQMLWLTAMYQGLKAATYFWPSSEVAINGSPFSIYMPYNGSPFERRISTL 302 Db 294 EKENPENTKGEPIWTKYCGLKSCTPFWPGSDVLENLGIFEDIYKMYNGSPFEEIRLLAV 353
Qy	600	ITAVKVNLPGRPRVTLQKNDKDHCLLYREYVSGFKAMKMPKNSYTVPKGDTSLLP	659	Qy 303 LKWLDDPKAERPRPYTINYFEEPDSSGAGGPVSARYVKALOVVDHAFGMLMBEGLKQRNLH 362 Db 354 LQWNLQPLDPERPFTYTLYLEEDPSGHSISYGPSSSEVTKAQLQVDGMVGLMDGLKELNLH 413
Qy	660	TVPDCLRADYRVPSPESQKCSFYLADKNTITHGFLYPASPNTSPSQTDALITSNLVPMYE	719	Qy 363 NCVNTILLADHGMDQTYCNKMYMTDFPRINFYMEGCPAPRIBAHNTIHDFFPENSB 422 Db 414 RCNLNLISDHGMEQGSCKKTYLYNCKLGDKVNKNVYGFPAARLKPSPDVDPKYSFNYBG 473
Db	660	TVPDCLRADYRVPSPESQKCSFYLADQNDHGFLYPPAIGKNEQSDALITSNLVPMYE	719	Qy 423 IVRNLSCKRPDQHFKPYLTDPKPLHYAKNVRIDKVLHFDQW-LAVRSKSNTNCGSG 481 Db 474 TARNLSCHEPQNQFKPLKHFPKPLHYAKNVRIDKVLHFDQW-LAVRSKSNTNCGSG 533
Qy	720	EFRKMDYFHSSVLKHTGATERBNGVNVSPGIFDYNYGHFDADEBITHLANTDVP1PTH	779	Qy 482 NHGYNNEFRSMEAIPLAIGPSFKEKTYEPFENIEVNLMCDLIRIOPADNGTHGSLNH 541 Db 534 FHSQDNVLSNMQALFVGPGPKHGEADTENIYNMCDLIRIOPADNGTHGSLNH 593
Db	720	EFRKMDYFHSSVLKHTGATERBNGVNVSPGIFDYNYGHFDAPEITINVAGTDVPTPH	779	Qy 542 LLKVPFYPEPSHAEBVKSFVCGFANPLPTESDLDCFC-PHLQNSTOLEVNQMLNLTQEII 600 Db 594 LLKVPVTPKHPKRVPLVQCBPTRN-PRDNLGCNSNPSI---LPIEDFOTQPNLTVABE 649
Qy	780	YFVVLTSCKNSKSHTPENCPSGMVLDFLPFIITPHTPTVNESEPEGKPEALWVEERFTAHTARY	839	Qy 601 TATVKVNLPGRPRVTLQKNDKDHCLLYREYVSGFKAMKMPKNSYTVPKGDTSLLP
Db	780	YFVVLTSCKNSKSHTPENCPSGMVLDFLPFIITPHTPTVNESEPEGKPEALWVEERFTAHTARY	839	Db 650 KLIKHETLPYGRVRVLCENTICLQSLQHOMGSGSDLQMLPLWTVYDVR--NDSFSTD 707
Qy	840	RDVELLTGLDYQDKYQPVSEBILQKTYLPTFETII 875		Qy 661 VPDCLRADYRVPSPESQKCSFYLADKNTITHGFLYPBPASNRTSDQY-DALITSNLVPMYE 719
Db	840	RDVELLTGLDYQDKYQPVSEBILQKTYLPTFETII 875		Db 708 FSNLQYOFRIPLSPVIRCSFYTNNNTKVSYFLSPQLNQNSG1YSEAUALLTIVPMYQ 767
RESULT 2				Db 720 EFRKMDYFHSSVLKHTGATERBNGVNVSPGIFDYNYGHFDAPEITINVNMCDLIRIOPADNGTHGSLNH 593
A39216		nucleotide diphosphatase (EC 3.6.1.9) - human		Db 720 EFRKMDYFHSSVLKHTGATERBNGVNVSPGIFDYNYGHFDAPEITINVNMCDLIRIOPADNGTHGSLNH 593
N	Contains: nucleotide Pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1.)			Db 768 SFQVITYRWFHDTRLKRKAERGVNTQVNGVSPFQDFDGRCDSLENLRQKRVINQOEILLI 827
C	Species: Homo sapiens (man)			Qy 777 PTHFPTVLSCKNSKSHTPENCPSGMVLDFLPFIITPHTPTVNESEPEGKPEALWVEERFTAHTARY
C	Accession: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 03-Jun-2002			A; Accession: S23587 A; Molecule type: protein A; Residues: 116-121,247-271,'X',273-275;279-280,'X',282-283;303-316;362-364,449-465,482- A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-925 <BEI>
R	Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Goding, J.W.			A; Note: it is uncertain whether Met-1 or Met-53 is the initiator R; Belli, S.I.; Goding, J.W.
J	Arch. Biochem. Biophys. 295, 180-187, 1992			Db 760 KLIKHETLPYGRVRVLCENTICLQSLQHOMGSGSDLQMLPLWTVYDVR--NDSFSTD 707
A	Title: Plasma cell membrane glycoprotein PC-1, cDNA cloning of the human molecule, amino acid sequence number: A39216; MUID:51009202; PMID:221644			A; Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase. A; Reference number: S21706; MUID:22246539; PMID:131502
A	Accession: A39216			A; Accession: S21706 A; Molecule type: mRNA A; Residues: 1-925 <BEI>
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A	Residues: 1-325 <UNL1>			A; Residues: 1-325 <UNL1>
A	Accession: S23587			A; Accession: S23587 A; Status: not compared with conceptual translation
A	Molecule type: protein			A; Molecule type: protein
A	Residues: 116-121,247-271,'X',273-275;279-280,'X',282-283;303-316;362-364,449-465,482-			A; Residues: 116-121,247-271,'X',273-275;279-280,'X',282-283;303-316;362-364,449-465,482-
Qy	720	EFRKMDYFHSSVLKHTGATERBNGVNVSPGIFDYNYGHFDAPEITINVNMCDLIRIOPADNGTHGSLNH 593		A; Note: it is uncertain whether Met-1 or Met-53 is the initiator R; Belli, S.I.; Goding, J.W.
Db	768	SFQVITYRWFHDTRLKRKAERGVNTQVNGVSPFQDFDGRCDSLENLRQKRVINQOEILLI 827		Eur. J. Biochem. 226, 433-443, 1994
Qy	777	PTHFPTVLSCKNSKSHTPENCPSGMVLDFLPFIITPHTPTVNESEPEGKPEALWVEERFTAHTARY		A; Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline phosphatase activity A; Reference number: S51030; MUID:95094801; PMID:801561
A	Accession: S51030			A; Accession: S51030

Db	828	PTHFFFTVLTSCCKDTQPLHCEEN-LDYLAFILPHRTDNSESCVHGKHDSSWVEELMLHR	886	Qy	300	STLKLWDLPKAERPRFYTMYFEEPDSSGHAGGPASRVITALQVWDHAFGMLMEGLKQR	359
Qy	837	ARVDVVELLTGLDFYDKVKQPVSEIIOLKTKLPTF	871	Db	333	LAVIEWLQLPSHERRPHPTTLYLEEDPSGSHSQGVSSSEVITALQVDRVGMMDGKDL	392
Db	887	ARITDEHITGUSFYQORKKEPVSDILKLKTHLPTF	921	Qy	360	NLHCNCVNTILLADHGMDDOTYCNCRMEYMTDYPRINFFYMEYGPAPIRAHNI-PHDFFSFN	419
RESULT 3	A27410	A27410 diphosphatase (EC 3.6.1.9) - mouse nucleotide diphosphatase (EC 3.6.1.9) - mouse phosphodiesterase I (EC 3.1.1.1)		Db	393	GLDKCLNLILLISDHGMEOQSCKXVYLINKYLGDNVNVKVVGDPAARURPTDVETYSFN	452
C;Species: Mus musculus (house mouse)	C;Accession: A27410; 159055; S38354	C;Date: 10-Sep-1999 #sequence 10-Sep-1999 #text_change 03-Jun-2002	Qy	420	SEEIVNLSCKRKPDQHEKPYLTDPKLRYAXNRVLDKVLHVFDQW-LAVRSKNTNC	478	
Rivan Driel, T.R.; Goding, J.W.	J.Biol.Chem. 262, 4882-4887, 1987	A;Title: Primary structure deduced from cDNA c1c	Db	453	YEALAKNLSCKREPKHQFLPQLHAKSDRIEPLTFDLPQWQALNPSEKRC	512	
A;Reference number: A27410; MUID:87165905; PMID:3104326	A;Accession: A27410	A;Molecule type: mRNA	Qy	479	GGGNHGYNNFRMSMAIFIAGHPSPEKKEVPPFTEVYNLMCDLRLICPAPEPNNGTHGS	538	
A;Residues: 1-905 <VAN>	A;Cross-references: GB:J02700; NID:G200216; PID:AAA39893.1; PID:g200237	A;Note: The authors transcribed the codon CAG for residue 24 as Glu	Db	513	GSGPHGSNDLFSNNOALFGYGAFLKGAEVSFENTEVYNLMCDLIGLICPAPENNGSGS	572	
Rivan Driel, T.R.; Goding, J.W.	PROC.NATL.ACAD.SCI.U.S.A. 82, 8619-8623, 1985	A;Title: Murine plasma cell membrane glycoprotein PC-1: Molecular cloning of cDNA and analysis	Qy	539	LNHLLKVPYEPHAAEVSKFSVCGFANPLPTESLDCFCPHLONSTOLEQNQMLNLTOE	598	
A;Reference number: 159055; MUID:87165905; PMID:3001713	A;Accession: 159055	A;Status: Preliminary, translated from GB/EMBL/DDJB	Db	573	LNLHLLKVPYNSPKHPSKEBGFSLSC---PIKTSNDLIGCTCDFWIVPKDFKQLNLTE	628	
A;Molecule type: mRNA	A;Cross-references: GB:J02700; NID:G200216; PID:AAA39893.1; PID:g200235	A;Residues: 1-905 <VAN>	Qy	599	EITATVKVNLPGRPRVILQPKVNDHCLLYHREYVSGFGKAMRMVMMWSYTVQPGDTSFLP	658	
Rivan Driel, T.R.; Goding, J.W.	EUR.J.BIOCHEM. 217, 421-428, 1993	A;Title: Identification and characterization of a soluble form of the plasma cell membrane antigen PC-1: Molecular cloning of cDNA and analysis	Db	629	D-DDTYRHMTPYGGDRILLKQHNVLLQQQFPLTGSIDLMLPLWASYTF-LRNQFSR	685	
A;Reference number: 159055; MUID:87165905; PMID:3001713	A;Accession: 159055	A;Status: Preliminary, translated from GB/EMBL/DDJB	Qy	659	PTVPPDCLRADVYRPPSESOKCSFYLAQDKNITHGFLYPPASNRTSDSQY-DALITSNLVPM	717	
A;Molecule type: mRNA	A;Cross-references: GB:J02700; NID:G200216; PID:AAA39893.1; PID:g200235	A;Residues: 1-905 <VAN>	Db	686	DDFSNCMYPDLRIPSPVRCSTSYYKNSKLSYGLTPPDLNRVSNHTISEALLTSNIPM	745	
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R.Belli, S.I.; van Driel, T.R.; Goding, J.W.	EUR.J.BIOCHEM. 217, 421-428, 1993	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	Db	746	YQSFQVIVWYLHDTTLQRYAHERNGINVSVGPVEDDYGRTSLELKIQNSNSVIRSOI	805	
A;Title: Identification and characterization of a soluble form of the plasma cell membrane antigen PC-1: Molecular cloning of cDNA and analysis	A;Reference number: S838354; MUID:94039066; PMID:8223581	A;Status: Preliminary	Qy	775	PIPTYFVFLTSCKNSKHTPENCQGLDVLPLFIPHRPTNIVESCPGKPEALVVERFTA	834	
A;Accession: S838354	A;Molecule type: DNA	A;Accession: S838354	Db	806	LIPPFEFFVLTSCSKQLSSEPLECSA-LESSAYLPHRPNTIESTGREGSSWAEELTL	864	
A;Cross-references: GB:J02700; NID:G200235	A;Cross-references: EMBL:LO4516	A;Status: Preliminary	Qy	835	HIAARYDVEILTGFLYQDKYQDVKQPVSEILOQRTVLPTE	871	
A;Molecule type: DNA	A;Cross-references: EMBL:LO4516	A;Status: Preliminary	Db	865	HRARYDVEILTGFLSYQDQESVSELLRKTHLPIF	901	
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Rivan Driel, T.R.; Goding, J.W.	Rivan Driel, T.R.; Goding, J.W.	Rivan Driel, T.R.; Goding, J.W.	C;Keywords: coenzyme A; glycoprotein; phosphoprotein; somatomedin B homology				
EUR.J.BIOCHEM. 217, 421-428, 1993	EUR.J.BIOCHEM. 217, 421-428, 1993	EUR.J.BIOCHEM. 217, 421-428, 1993	C;Species: Rattus norvegicus (Norway rat)				
A;Title: Identification and characterization of a soluble form of the plasma cell membrane antigen PC-1: Molecular cloning of cDNA and analysis	A;Reference number: S838354; MUID:94039066; PMID:8223581	A;Status: Preliminary	C;Date: 10-Sep-1999 #sequence 10-Sep-1999 #text_change 03-Jun-2002				
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A;Molecule type: DNA	A;Molecule type: DNA	A;Molecule type: DNA	R;Narita, M.; Goji, J.; Nakamura, H.; Sano, K.				
A;Cross-references: GB:J02700; NID:G200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	J;Biol.Chem. 269, 2823-2842, 1994				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Description: Cloning and expression of brain-specific phosphodiesterase				
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A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Description: Cloning and expression of brain-specific phosphodiesterase				
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A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	R;Narita, M.; Goji, J.; Nakamura, H.; Sano, K.				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	C;Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphor diester hy				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	F;54-97/Domain: somatomedin B homology <SBH1>				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	F;58-141/Domain: somatomedin B homology <SBH2>				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	F;53-150/348-405/522-608-829/Binding site: carbohydrate (Asn) (covalent) #status predicted				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	F;207/Binding site: AMP (Thr) (covalent) #status predicted				
A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	A;Cross-references: GB:J02700; NID:G200234; PID:AAA39892.1; PID:g200235	Query Match	42.5%	Score 2043.5;	DB 1;	Length 885;

Best Local Similarity 41.7%; Pred. No. 6.8e-135; Indels 79; Gaps 12; Matches 380; Conservative 178; Mismatches 275;

Qy 14 KRNLLKKYIACIVLALLIVMSIGLGIGLRKLEK-----QGSC 54
 Db 3 RQCGGSFQVSLITFAI----SYNICLGFATSRKIAEWDEGGPTVLSDEPWTNTSGSC 58
 Qy 55 RKCFEDASSRGLENCRDVAACKDRGDCCWDFBDTCVESTRMCNKFRGEIRLEASLCS 114
 Db 59 KGRCFELQEVGPDCRDNLCKSYSSCCDDEBLCLTKVGECTDRSGEVRENEACH 118
 Qy 115 CSDDQLQKEDCAYDKSVEGETSWLEENCDTAQQSOCPEGFDL--PPVLFMSMDGFRAE 172
 Db 119 CPEDCLSRSDCCCTNQVQVGKGEHWW---DDAARNOSBCLQVCQPPLIFSVDFGRAS 174
 Qy 173 YLYTWDLIMPNTINKLKTCGHSKYMRAAMYPTKTFPHNYTIVGLEYPSHGIDDNNNYDVN 232
 Db 175 YMKGSKVMPNIEKLRSCTTHVTRPYPTKTFPNLYTATGLEYPSHGIGTVGNSMTDPV 234
 Qy 233 LNKNFSLSSEKEQNPAWTHGQPMWLTAMYQGLKAATYFWPGSEVAINGSPSISIMPYNGS 292
 Db 235 FDASFHLREKEENHRHWRGKQPLWITAKQYTRAGIFFW-----SVS 276
 Qy 293 VPFFERISTLKLWDLPKAERPFYIINYFEEPISSGAGGPPYSARTIKALOYVDIRFGML 352
 Db 277 IPHERRILTLQWLSLPLNERPSVAYTSEQFESGHKYKGFEGPENTNPLREIDTKVGQI 336
 Qy 353 MEGLRORNHNCCNNTILLADHGMDOTYCNKMEYMTDFPRINFFYMEYGAPEPRAHNTP 412
 Db 337 MDGKQCLPLHRCVNPVIFQDHMDEVDTDRTEFLSNLNTINDITIVGTLGRFAKSIN 396
 Qy 413 HDFFSFNSEEIVNLSCRKDPOHDFKPTLPDLPKRLHYAKVNDRIDKVLFYDQON---- 467
 Db 397 NS--KYDXTTIANLICKKPDKDOKPKNQHPKRUHYANRRIEDHLVDRRHVAIK 454
 Qy 468 -LAVERSKNNTNC-GGHHGKYNNEFRSMEAATLAHGDSRKETTEBRENTEVNLMDL 525
 Db 455 PLOVKCESGKCFQGDHGDKNVSNQTVFVGYGPFKRTKVPFENELVNWMCQJL 514
 Qy 526 RIQAPAWNGTHGSINHLIKVPPYEPSHAEVSKESVCGFANPLPESLDPCF-PHLQNST 584
 Db 515 GIKPAPWNGTHGSINHLRHTTFRPMDVEVSRPNYGMYQSEFDGTCDDKVEPKPN 574
 Qy 585 QLEQVNQMLN-----TOBETATVKV---NLPFGVRVLQRNVHDIC 623
 Db 575 KLEELNRKLTGKGSTEATGKFRGSKHENKNLNGSVEPKERHLYGRBAVLXR-TSYD 633
 Qy 624 LLYHRETVSGFGRAMMPMWSSYYTVPQLGDTSPPLPPTVPCDLRADVRVPPSESOKCSFYL 683
 Db 634 ILYHTDEGSISEBFMLPLTSYTISKQAEVSSIPHEHLTCVRPDVSGFSNCLAVK 693
 Qy 684 ADDNTHIGFLPPASNRTSDSOYDALITSNLYPMBEFROMWDYFHSVLLIKHATERNSY 743
 Db 694 NDQKOMSTGFLFPPYLSPEAKYDAPLVTKNVPMPAFKSWAYFQRLVTKYASERNKV 753
 Qy 744 NYVSGPFDYDNNYDGHFDAPEDETKHLANTDVPITHYFVUTSKANKSHTPENCPGMLDV 803
 Db 754 NVISGPFDNYDGYDLDTEDIKOYEGSSIPVPIHYSSITSCHDFTQPADKCDGPLSV 813
 Qy 804 LPFLIPIRPRPTVNECSCPEGKPAALWTEERTAHIANVRDVELLGIDFYQDKVQPVSELQ 863
 Db 814 SSFILPHERPNDDESCNSSEDESKVYEBLMQHETARVRDIEHLTGLDFYKTKTSYSSEBLT 873
 Qy 864 LKTYLPTFETTI 875
 Db 874 LKTYLHTYESEI 885

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A55144; A4329
 R;Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.B.; Liotta, J.; Biol. Chem. 269, 30419-30484, 1994
 A;Title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveal
 A;Reference number: A55144; PMID: 95074054; MUID: 95074054
 A;Molecule type: protein
 A;Residues: 1-915 [**MUR**]
 A;Cross-references: GB:L35594; NID:G537905; PID:AA647851; PMID:G537906
 A;Note: Parts of this sequence were confirmed by peptide sequencing
 R;Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cioce, V.; Schiffmann, E.; J. Biol. Chem. 267, 2521-2529, 1992
 A;Accession: A4329; A55144
 A;Title: Identification, purification, and partial sequence analysis of autotaxin, a novel
 A;Reference number: A4329; MUID: 92129337; PMID: 1733949
 A;Accession: A4329
 A;Molecule type: protein
 A;Gene: GDB:ATX
 A;Cross-references: GDB: 378346
 A;Map position: 8q22-8qter
 A;Extracellular source: A2058 melanoma cells
 C;SuperFamily: nucleotide pyrophosphatase; somatomedin B homology
 C;Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
 F:55_98/Domain: somatomedin B homology <SBH1>
 F:54_463_577_859/Binding site: carbonylate (Asn) (covalent)
 F:54_463_577_859/Binding site: AMP (Trir) (covalent)
 C;Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
 C;Genetics:

A;Gene: GDB:ATX
 A;Cross-references: GDB: 378346
 A;Map position: 8q22-8qter
 A;Extracellular source: A2058 melanoma cells
 C;SuperFamily: nucleotide pyrophosphatase; somatomedin B homology
 C;Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
 F:55_98/Domain: somatomedin B homology <SBH1>
 F:54_463_577_859/Binding site: carbonylate (Asn) (covalent)
 F:54_463_577_859/Binding site: AMP (Trir) (covalent)
 C;Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.

Query Match 42.5%; Score 2040.5; DB 1; Length 915;
 Best Local Similarity 40.5%; Pred. No. 1.2e-135;
 Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps 11;

Qy 24 ACIVLALLIVNSIGLGLGLRKLER-----
 Db 9 SCQISLFLTFAVVSICLGFATTAHKIREAEGWBEGPPTVLSDPWTNISGSCKGRCPFLQE 68

Query Match 42.5%; Score 2040.5; DB 1; Length 915;
 Best Local Similarity 40.5%; Pred. No. 1.2e-135;
 Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps 11;

Qy 64 RGCLENCDVACKDGRGCCWDPEDTCVESTRIMCNKFRGCTRLASLGSQDDLQKR 123
 Db 69 AGPBDRCDDNLCKSYTSCHDDELCKTARGWECKDRCGEVRNEACHSEDCLARG 128

Qy 124 DCDAIKSVCGQGETSWIENCDTAQQQCQCBPFBFDLPPVILESMMDGPRAEYLYTWDTLMPN 183
 Db 129 DCCTNYQVCKESEHWDDCBEIKAKACPGFVRPLIIISVQFPRASMKGSKMPN 188

Qy 184 INFLEKTCIHSYKTMRYNPTKTFPNTYHITYTGLYPHESHGIDNNNNYDVNLKNFNSLSKE 243
 Db 189 TEKLRSGTCHSPYMRPVPTKTFPNTLYTATGLYPHSGHIVGNSMYPVFDATFHGRE 248

Qy 244 ONNPWVHGQPKWMLTANYQGLKAATYFWPGSEVAINGSFSPSIYMPYNSYFPEERLSTLJ 303
 Db 249 KENHRWGGQWPWITAKQVAGTFPW-----SVPVHP-----ERRITIL 290

Qy 304 KNIDLPLKAERPRFTYMFEEPDSSCHAGGPVSA-----
 Db 231 RWATLPLDHERPSSVAYFSEQBDFSKYKGPFGPEESESSYGSFAPRIR--AHNIPHDFFSFNSEEIVRNRLS 428

Qy 337 -----RVIKALQVVDHAFGMLMEEGLKQRMNLHNCVNLILLA 371
 Db 351 PVAPPKXRRKIHMRDMHYYAETRQDMTNPLREIUKVGLMDGKQLKQKLRRCYVIFVG 410

Qy 372 DHGMDQTYCNRKEMDYDFPSINFFYMEGAPRIR--AHNIPHDFFSFNSEEIVRNRLS 428

Db 411 DHGMDVTCRDTFEELSNVNTDDITLVPGLGRSKFENAKYD---PKAIIANLT 465

Qy 429 CRKPDQHFKFPLTPDPLKRLHYAKVNRDVKHLFYDQW----LAVRSKSNTNC-GGG 481

Qy 466 CKKPQDFKFPLKQHLPKRHYANRRIEDHLLVERWEVARPLDVKKPSGKCFQG 525

RESULT 5
 A55144
 autotaxin precursor - human
 N;Contains: phosphodiesterase I (EC 3.1.4.1)
 C;Species: Homo sapiens (man)

Qy	482 NFGYNNPFRSMBAIFLAHPGPFKEXTTEVEPPENIVNACDLRIOPAPNNNGPHGSLNH 541	Qy	448 LHYAKNVRIDKVHLFDQMLAVRSKRANTNCGGNHGNNEPRSMEAIFLAHPGPSEKEKT 507
Db	526 DHGFDNKVNNSMGTQFVGYGPFTKVKVPPNENIYLNNCKLGPKNNGTHGSLNH 585	Db	397 LHYDSDRIPPIGLDEGEKYEOKSKAKECGGAHYDNAAFSMRTTIFGHGMPMSKGR 456
Qy	542 LLRKVPFPVSHAEVSKSVCGFANPLPTEISLDCCF- PHILONSTOLEQNQMNLTQEII 600	Qy	508 EVEPENIEVNLIMCDLRLIQPAPNGT 535
Db	586 LIRNTNTRPTMEBEVTRNPYPRIMQLSDFDGLCTDDKYEPKPNKLDELNKRLLTK- --- 641	Db	457 KVPSFENQJYNVISILGLKAPNNGS 484
Qy	601 TATVKVNLPLFGRPRVLRQNDHCLLYTREYSGKAMRMWSSVTPQLGDTSPPLPT 660	RESULT 7	
Db	642 GSTEERHLILYGRPAVLX-TRYDILHTDPESGYSEIFLMWLWTSVTSRQAEVVSPDH 700	TO3233	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) - rice
Qy	661 VPDCLRRAVRYRVESEOSCRCSPTLADNTLTSNLSLNSYPMYE 720	C;Species: Oryza sativa (rice)	
Db	701 LISCVRPPRVRVSFSQNCLAYKNDKOMSYGTLFPYLISSPEAKYDAFLYTNKMPYPA 760	C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Aug-2002	
Qy	721 FKKWQDYFHSVLLIKHATERGVNVVSGPFDYNYDGHFADPELTKHLLANTDVPIPTHY 780	C;Accession: T03233	
Db	761 FKKWQWYFQRLVYKQYASERNGVNISCPFIFYDGLHDTEDKQKYVESSIPPHY 820	A;Description: Rice early embryogenesis gene.	
Qy	781 FVVLTSCKNKSHTPENCHGWLDPFLPHRPTNVSCPEGKPEALWVEERTTAHTARY 840	A;Reference number: Z14889	
Db	821 YSLITSCLDFTQPADKCGCPLSVSSFTPHRDNEESCNSSDESKVVEELMKHTRVR 880	A;Accession: T03293	
Qy	841 DVEBLTGGDFYQDKVQPSFELQOLKTYLPTFETI 875	A;Status: translated from GB/EMBL/DDBJ	
Db	881 DIEBLTSLDFEKTSTSYPEILTLYLTYSEBI 915	A;Molecule type: mRNA	
		A;Residues: 1-479 <HSI>	
		A;Cross-references: EMBL:U25130; NID:5818848; PID:9818849	
		A;Experimental source: strain Tatnun 67	
		C;Genetics:	
		C;Gene: OSB4	
		C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4	
		C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase	
		Query Match 15.4%; Score 737.5; DB 2; Length 479;	
		Best Local Similarity 42.0%; Pred. No. 3.4e-44;	
		Matches 163; Conservative 64; Mismatches 140; Indels 21; Gaps 10;	
Qy	TO931 PROBABLE PHOSPHODIESTERASE I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4 .	Qy	159 PPVILFSMDGFRAEYLTYWTMLPINKLKTCGIIHSY-MRAMYPTKTFPNHYTTVTGLEY 217
C;Species: Arabidopsis thaliana (mouse-ear cress)	C;Accession: T0931	Db	90 PVVILISSDGRFGHQHAA-T-PHHLRIGNTGTSATGLVPIPFITLPBNHYSATGLEY 147
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002	C;Accession: TO931	Qy	218 PESHGIDINMYDYNKNSLSSKEQNPNPAWWHIGOPMLTAMYCGLKRAATYFWGSEVA 277
C;Reference number: TO931	C;Accession: TO931	Db	148 PSSHGILINNYFPDPISGQDYMSSHE--PKWNLISPLVTAADDQIAQATYFWGSEVK 204
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X	R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X	Qy	278 INGSF--PSIV-MPINGSVPEERSTLKLWDISKKAERPRFTYMFEEBDSSGHAGGPV 334
submitted to the Protein Sequence Database, June 1999	submitted to the Protein Sequence Database, June 1999	Db	205 -KGSMDCPDKYCRHATGNSVPEERSTLKLWDISKKAERPRFTYMFEEBDSSGHAGGPV 447
A;Experiment number: Z16897	A;Experiment number: Z16897	Qy	335 SARVITALQVYDHAFLMELGKQNLHNHCVNIIILADHGMDQTWCNKRMKBYMTDXFPRIN 394
A;Accession: TO931	A;Accession: TO931	Db	324 LBEDWVLSMTPLLAIR---PPDDMSLPLDVYARNEGLGSCKVENGYLMLKDPLPSR 379
A;Molecule type: DNA	A;Molecule type: DNA	Qy	448 IHYAKNVRIDKVHLFDQMLAVRSKSNTNGCGNHGNNEPRSMEAIFLAHPGPSEKEKT 507
A;Residues: 1-496 <BEV>	A;Residues: 1-496 <BEV>	Db	380 LYADSTRIPPILGPPEGYKEMRSKDNKGAGYDNAFFSMTTIFAHGPRFEGGR 439
A;Cross-references: EMBL:AL079344; GSDB:GN00062; ATSP:T16L4.190	A;Cross-references: EMBL:AL079344; GSDB:GN00062; ATSP:T16L4.190	Qy	508 EVEPENIEVNLIMCDLRLIQPAPNGT 535
A;Experimental source: Cultivar Columbia; BAC clone T16L4	A;Experimental source: Cultivar Columbia; BAC clone T16L4	Db	440 VYPSFENEVIVNVIASLNLFPAPNNGS 467
C;Genetics:	C;Genetics:	RESULT 8	
Qy	157 DLPPVILFSMDGFRAEYLTYWTMLPINKLKTCGIIHSY-MRAMYPTKTFPNHYTTVTG 215	TO932	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4
Db	105 DKPVVLLISSDGFR--FGIQFKTKLPSHLRIANGTEATGLPVFPTLFPHYSITG 162	C;Species: Arabidopsis thaliana (mouse-ear cress)	
Qy	216 LYPSBRGIDINMYVNLNKNFSLSSKEQNPNPAWWHGPMLWAMYQGIKAATYFWPOSE 275	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002	
Db	163 LYPATGIIINHHFVDPETGNVFTMASHE---PEWNLGEPIWETVNGLKKAATYFWPOSE 219	C;Accession: T0932	
Qy	276 VAINGSF---PSIYMPYNGSVPEERSTLKLWDLPLCAERPRFTYMFEEPDLSGHAGG 332	C;Reference to the Protein Sequence Database, June 1999	
Db	220 VH-KGWNCPGGLCONYGSVPEERSTLKLWDLPLCAERPRFTYMFEEPDLSGHAGG 278	A;Accession: T0932	
Qy	333 PVSARYTKALQVVDHAFGMMEGLKQRNLHNCVNLLADHGMDQTCNKMEYMTDXFPR 392	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4	
Db	279 PDDPQITEAVNIDRJGRGLDGLERGIFDVTMVGHGMVTCRDKLVLVDDLPLPSR 358	C;Species: Arabidopsis thaliana (mouse-ear cress)	
Qy	393 INF---FYMFGPAPRRAHNIPHDEFSENSEEIVNLSORKPD--CHFKPYLTDPLPKR 447	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002	
Db	339 IKIPSSWVQYXTPLAIOPPS-GHDAADIVA-KINEGLSSGKVENGKLVKLVKEDLPSR 396	C;Accession: T0932	

A;Molecule type: DNA A;Residues: 1-457 <BEV> A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4 .200 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Accession: T0933 R;Bevan, M.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X. A;Reference number: Z16897 A;Molecule type: DNA A;Residues: 1-161 <BEV> A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4 .210 C;Genetics: C;Experimental source: cultivar Columbia; BAC clone T16L4 A;Gene: ATSP:T16L4 .210 A;Map position: 4 C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4 C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase	Db 58 PVTMLISCDGFRFGYQEKDT - PNIDLLISGGTEAKHGLIIPVFPPTMTPNHYSIATGLY 115 Qy 218 PESHGIDDNMMYDVNINNKNSLSSKEQNNDPAWHEGQPMWLTAMYQGLKATYFPGSEVA 277 Db 116 PAYHGIMNKFTDPVGEVNGKQ - - PKWNLGEPLWVTAQNGLKAVTYFWPGSEVA 171 Db 278 ING-SEPSIIMP-TNGSVPEERISTLKLWDLKAERFRFTYMFEEBDSSGHAGGPVS 335 Qy 172 KSSWTCPBGTCPHENULSVPLEERVDSVLSHFDLDEVEDPDLMLYFDEPDQSHNYGDD 231 Db 336 ARVIAKQVDHAFGLMELKGQLNHNCTNITLADHM-DQTCYCNKMEYNTDYPFRI 393 Qy 232 PRVTAWSVSDKMRGVIKLGKQREIFDEVHVLGDMVNTCNEKAYIDDLADI 291 Db 394 NFFYMYEGPAPRRAHNIPHDFFFSNE ----- EVRNLSCR - - - - - KPDQ 434 Db 292 KI - - - - PAWICAYS - - - - - FVLAIPNPGKDVENQSERNAEVAKMNEALSGGKVNGE 342 Qy 435 HFKPVLTPDPLPKRLHYAKNVRDKVHLFVDQQLAVRSKSNTNCGGMHGYNNEFRSMEA 494 Db 343 FLKVYLGKELPERLHSSEYRIPPIGIVGIMVRQNTNAQCVYCQGDHGYNELFMSRT 402 Qy 495 IFLANGSPFEKTEVEPENITYPNLMDLLRQPAENG 535 Db 403 IFVGHGGSRSRGKXPSFENQVYNNVAELLGURPANNNG 443
RESULT 10 A5930 Probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) 5 - monomer N;Alternative names: ectonucleotide pyrophosphatase/phosphodiesterase 5; NPP5 C;Species: Mus musculus (house mouse) C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2002 C;Accession: A5930 R;Gibbersen, R.; Ceulmans, H.; Stalmans, W.; Bollen, M. J. Biol. Chem. 276:1361-1368, 2001 A;Title: Structural and catalytic similarities between nucleotide pyrophosphatases/phosphatases A;Reference number: A5930 A;Accession: A5930 A;Molecule type: DNA A;Residues: 1-477 <GI> A;Cross references: GB:AF233377; NID:912231525; PINN:AA494913.1	Qy 363 MEYMTDYFPRINFFYMYEGPAPRRAHNIPHDFFFSN - - - - - SBEIVRN - - 426 Db 277 VITDDILAWIKI - - - - - PADWODYS - - - - - Db 427 -LSCRK- PDQHKPKVLTDPDPLPKRLHYAKNVRDKVHLFVDQQLAVRSKSNTNCGGNH 483 Qy 328 AUSSGKVANGEFHQVQLKENLQRHLYSDDSSRPIPLIGMGEGLMVKQNRVYYQECSGTH 387 Qy 484 GYNNEFRMNEAFLAHGSPSFKERTVEPENITYPNLMDLLRQPAENGTHGLSLNHU 543 Db 388 GVDNMFFSMSRSI FVGYGPRFRGKVPSEENTQVINAELGLRPAAPNGSSLTRSLI 447 Qy 544 KVPFYEPHAE 554 Db 448 -LPFGERTSQVE 457
RESULT 11 A5930 Probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4 . C;Species: Arabidopsis thaliana (mouse-ear cress) C;Accession: T0933 R;Bevan, M.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X. A;Reference number: Z16897 A;Molecule type: DNA A;Residues: 1-161 <BEV> A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4 .210 C;Genetics: C;Experimental source: cultivar Columbia; BAC clone T16L4 A;Gene: ATSP:T16L4 .210 A;Map position: 4 C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4 C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase	Db 144 CDTAQQSQCPEGFDLPPVILSMGDGRAEYLWTDLMPNINKLKTGIGHNVQNTVNPFI 203 Qy 16 CHSAPFISQPEE - - - QVLYSPDGFRWDLYKVPT - - PHFYIMKNQGVHNVQNTVNPFI 70 Db 204 KTFPNHNTTGTOLYPEHGLIDNNMVDNLNNKNSLSKSE QNNPAWWHQPMWLTAMYQ 262 Db 71 KTYPNHNTLVLGFANHGTVANDMDPLINKSFSLEHMIYDSKFWEETPWIWINQRA 130 Db 263 GKAATTFWPGSEVAINGSFSTIYMFYEGPAPRRAHNIPHDFFSENSEIYSTLKWLDLPAERP - RYTMVF 321 Db 131 GHASGAMWPGRDKVHKDSFPPVYLPPNEYESFEDRVAKIEWP -- TAKDPINLGFLW 187 Db 322 EPBDSSCHAGGVSARVTKALQVWDHAFGMIMEGLKQRNLHNCVNLIIADHGMDOTYCN 381 Db 188 EPDDGQHVDPSLPGSVISDVKLGLIUMKRAWNWNLVTSDHGHTQCSRQ 247 Qy 382 KNEYMTDYFPRINFFYMYEGPAPRRAHNIPHDFFSENSEIYSTLKWLDLPAERP - RYTMVF 441 Db 248 RVIEDLRYLDKETHYLIDHSVAAI - - - LPKE - - - GKFDVYDALAGAHP - - NLTVYRK 298 Qy 442 PDLPKRLHYAKNVRDKVHLFVDQQLAVRSKSNTNCGGMHGYNNEFRSMEAFLANGP 501
RESULT 9 T0933 Probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4 . C;Species: Arabidopsis thaliana (mouse-ear cress) C;Accession: T0933 R;Bevan, M.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X. A;Reference number: Z16897 A;Molecule type: DNA A;Residues: 1-161 <BEV> A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4 .210 C;Genetics: C;Experimental source: cultivar Columbia; BAC clone T16L4 A;Gene: ATSP:T16L4 .210 A;Map position: 4 C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4 C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase	Qy 382 KNEYMTDYFPRINFFYMYEGPAPRRAHNIPHDFFSENSEIYSTLKWLDLPAERP - RYTMVF 441 Db 248 RVIEDLRYLDKETHYLIDHSVAAI - - - LPKE - - - GKFDVYDALAGAHP - - NLTVYRK 298 Qy 159 PPVILMSDGFRAEYLWTDLMPNINKLKTGIGHNVQNTVNPFI 217

Db	299 EETPERHYKHNDRVOPIVAVADEGWLQNKSD-DFLGNHGYDNALEMPIFLAHGP 357	
Qy	502 SPREKTEVEPPENIEVNLMDLLRIQDAPANGTHGSILNHLLIKVPPFPEHAEVSKFSV 561	A;Description: Contains actin, gamma pseudogene 9, a gene similar to PLASMA-CELL MEMBRAN
Db	358 APKNFTEAMMNTDLIULCHLNLLPAPLPHNGSFVNQDLL----- 399	A;Reference number: A59391
Db	562 CGFANPLPIESLDLDCFCPHQNSTQL 586	A;Molecule type: DNA
Qy	400 -SSATPKP-----IPTQSITL 416	A;Residues: 1-477 <SMA>
Db		A;Cross-references: GB:AU035701; NID:55924007; PIDN:CA56566.1 R;Gisberts, R.; Cellemans, H.; Stalmans, W.; Boilen, M. J. Biol. Chem. 276: 1361-1368, 2001
	RESULT 11	A;Title: Structural and catalytic similarities between nucleotide pyrophosphatases/phospha-
	T44657	A;Reference number: A59390; MUID:1125673; PMID:11027689
	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) SPBC72	A;Contents: annotation
	C;Species: Schizosaccharomyces pombe	A;Genetics: ENPP5
	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002	A;Map Position: 6p11.2-6p21.1
	C;Accession: T40657	C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase
	R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.	C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase
	submitted to the EMBL Data Library, November 1998	F72/Active site: Thr #status predicted
	A;Reference number: Z21889	Query Match 13.2%; Score 632.5; DB 1; Length 477;
	A;Accession: T40657	Best Local Similarity 34.4%; Pred. No. 8.6e-37;
	A;Status: translated from GB/EMBL/DDJB	Matches 140; Conservative 80; Mis.matches 154; Indels 33; Gaps 10;
	A;Residues: 1-485 <LYN>	Qy 156 FDLPP---VTLFSUDGFRAEYLTDIMPININKRGTGHSKMRAMYPTKTFPNHYT 211 Db 21 FSLQPDDQKVLVLSDFGRDYLYKVPY -PHEHYIMKGVHVGTVNVEITKTYFPNHYT 78
	A;Cross-references: EMBL:AL034352; PIDN:CAA22177.1; GSPPDB:GN00067; SPDB:SPBC725..05C	Qy 212 IVTGLYPSHSGIDINNMYDYNLNKNFSLSSKE-QNNPAWHGQPMWLTAMYOGIRAAATYF 270
	A;Experimental source: strain 972h-; cosmid c725	Db 79 LVTGLPAAENGIVANDMFDIRNKSFSLMMNITYSKFWEATIWITQRAGHTSGAA 138
	C;Genetics:	Qy 271 WPGSEYAIAGNSFPSTYMPYNGSVPPBEERISTLKLWDLPKAERPFPTFYMYFEEPSSGHA 330
	A;Gene: SPDB:SPBC725..05C	Db 139 WPGTDTKIHKREPTYHMPYMPYNSBSPDVRKIAE--FITSKEPNGLLWEDPDGMGH 196
	A;Map position: 2	Qy 331 GGPVSARVKIALQVHDHAFMLMEQLKORNHLNCUNLILADHNDQTYCNKMEYMTDF 390
	C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase	Db 197 LGPDSPLMGPVTSDDDKLGQYLNMKKAKLWNLTISDHANTQCSBERLIEDQYL 256
	C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase	Qy 391 PRINFFYMEYGPAPTRAHNIPHDSFSNSEBIVNLSCRKPDOFKPYLT---PDLPK 446
	Query Match 13.3%; Score 637; DB 2; Length 485;	Db 257 DKDHYLILQSPVAAI---LPEK---GKDEVYVLT----HAHPNLTVYKEDVPE 303
	Best Local Similarity 37.5%; Pred. No. 4.2e-37;	Db 134 HGIIDDNMMYDVNLNKNSLSSKNEON-NPAWM-HGQPMWLTAMYOGLKAAATYFWPGSEVAI 278
	Matches 146; Conservative 64; Mis.matches 165; Indels 14; Gaps 8;	Qy 447 RLHYAKNRVIRDKVHLFDQOOLAVRSKSNTNGGGNHNGTNNNEFRMEAFLHAGTSFKEK 506
Qy	161 VLFMSMDGFRAEYLTDLMPNTNCKTCGTHSKYMLAMYPTKTFPHYTTVTGLYPES 220	Db 304 RWHYKTNRSRIOPIAVADEGWHILQNSD-DFLQMGHGDNALADMHPFLHAGFAFRK 362
Db	76 VIVISLDGFRADLYRGGT--PNLSSLARNVHVPFLPSFSSITTPHYTTVTGLYPES 133	Qy 507 TEVEPENNIEVYNNIMCDLRLIQPAPNGNTHGSLNLHK-----VPF 547
Qy	221 HGIDDNMMYDVNLNKNSLSSKNEON-NPAWM-HGQPMWLTAMYOGLKAAATYFWPGSEVAI 278	Db 363 FSKEAMNSTDLYPLCHLNTITAMDHNGSPWNQDILNSAMPVVY 409
Db	134 HGIISNNFDFDVTQFSNMPENKDPTWWDGEPIVNAEENVRSAVHWPGNVEN 193	RESULT 13
Qy	279 NGSPPSIIMPYNGSVPPBEERISTLKLWDLPKAERPFPTFYMFEEPDSSGHAGGPYSARV 338	A11179
Db	194 HGYRTYSDGFNFDTTREKKDRDQLLAAZAPHDMVGHAFGPDEEL 253	protein kinase PC-1 (EC 2.7.1.-) - bovine (fragments)
Qy	339 IKALQDVIDHAFGMLMEGLKORNHLNCVNTILLADHGMQTYCNKMETYDYPINFYM 398	N;Alternate names: MAPF; major acidic fibroblast growth factor-stimulated phosphoprotein
Db	254 NIIQEVNDIVIGELIJEGLKERNIDKHVNNTIFLSDHGMWAPTSNDRLINDNMNLSAVHR 313	C;Species: Bos primigenius taurus (cattle)
Qy	399 YEGPAPRRAHNIPHDFFSNSEBIVNLSCRKPDPDKRLHYAKNVD 457	C;Date: 28-May-1992 #sequence_revision 22-Apr-1995 #text_change 30-Apr-1999
Db	314 DAWPLGGFRRGESDLDDEYY-ESLVNVYRSSLPSAENWNTVSKKD1FSRWHYNNERIA 371	R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
Qy	458 KVHLFVDQOLAV---RSKSNTNGGGNHYGYNNEFRSMEAFLPLAHPGSFK--EKTEVEP 511	J. Biol. Chem. 268, 27318-27326, 1993
Db	372 PVMMPDVGVSLVSMLDHSPELEYEPLGVYGDNLSPNRAFLTAGSSFKNPKFKLAP 431	A;Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein kinase
Qy	512 FEN1EVNNLMDLRLIQPAPNGNTH-GSL 539	A;Reference number: A41179; MUID:1715869
Db	432 FQNTFYGILSHILDPLAQNNGTYEGAL 460	A;Accession: A41179
	RESULT 12	A;Molecule type: protein
	A59391	A;Residues: 1-2636-56;59-67;68-133;134-144;145-267;268-300 <ODA>
	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) 5 - hu	R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
	N;Alternate names: ectonucleotide pyrophosphatase/phosphodiesterase 5; NPP5	J. Biol. Chem. 268, 27318-27326, 1993
	C;Species: Homo sapiens (man)	A;Title: The major acidic fibroblast growth factor (aFGF) -stimulated phosphoprotein from esterase activities
	C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2002	A;Reference number: A49308; MUID:94086550; PMID:7505270
	R;Smalley, C.	A;Accession: A49308

A;Molecule type: protein
A;Residues: 27-35, X, 37-58 <OD2>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:141583)
C;Superfamily: nucleotide pyrophosphatase / somatotomin B homology
C;Keywords: Glycoprotein; phosphotransferase; phosphotransferase
P;1_25/Domain: somatomedin B homology (fragment) <SBH>
F;36/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 13.2%; Score 632.; DB 2.; Length 300;
Best Local Similarity 21.8%; Pred. No. 4; DB 2.;
Matches 14; Conservative 51; Mismatches 71; Indels 504; Gaps 13;

Qy 57 KCFDASFRGLENCRCDVACKDRGDCCWDFDTCVESTRIMMNKFRGETLEASLSCS 116
Db 2 RCFERTF--GNCRCDAAEVGLNCCLD- 26

Qy 117 DDCDQKRQDCADYKSVCOETSMSLEENDTAQQSQCPBEGFDLPPVTLFSMDGFRAZLYT 176
Db 27 ----- 26

Qy 177 WDTLMPINRKLTKCGIHSKYMRYPTKTFPNHYTTIVTGLYPESHGIDNNMYDYNLNKN 236
Db 27 -----NMRPVYPTKTFPNHEYSIVTGLYPESHGIDNK----- 58

Qy 237 FSLSSKEQNTPAWHGQPMWLTAMYOGI-KAATYFWPGSEVAINGSFPSIYMPYNGSVPE 296
Db 59 -----GEPIWLTA----KSGCTFWPSSDVKINGIFDIXV--SVPE 95

Qy 297 ERISTLXWLDLPAERPRFYTMYFEEBDSSGHAGGVSAVRIKAQLQVWDHAEGMLMEGL 356
Db 96 ERLIAILKWLQLP----- 108

Qy 357 KORNLLHENCNVNIILLADHDMDQTYCNKMEYMTDYFPRINFTYMEGAPAPRRAHNTPHDF 416
Db 109 KELNLHRCNLNLILLSDHMGMEQSCK-----YY 135

Qy 417 SFNSBEITVRNLSCRKPDKDHFHKPYLTDLPKRLHYAKNVRDKVHLFVDQOM-LATRSKN 475
Db 136 SFDYEGI-----AKSDRERLTFYLDPPQQLAINPSE 168

Qy 476 TNCGGNHGHQYNEFRSMEAIFIHALGPFSFKETEVEPFENIEVYNNMCDLIRIOPAPNGT 535
Db 169 KYCGGFIGSDNLFNNOALFXXXXXXXHSTEVDSTENIEVYNNMCDLNLTPAPNGT 228

Qy 536 HGSUHLILKVPFVEPSPHAEVSKFSVGAPNLPLTESLDCFCPHLONSTOLEQVNQMLN 595
Db 229 H----- 229

Qy 596 TQEETATVKVLNPFGPRVQKNDVDEHCLTHREYVSGFGKAMRMFMWSSTVPOQGDT 655
Db 230 ----- 229

Qy 656 PLPPTVPDFCLRADVRVPSEOSOKCSFYLAQNTHTGFLYPASSNRTSDSY-DALITSNL 714
Db 230 -----LSYGFELSPQIHKCSSQYSEALLTNI 257

Qy 715 VPMYEERFKMDYFHSVLLKHATERNGVAVVSGP1FDNYTDGHEDAPDBITKLANTDV 774
Db 258 VPMYQSFQ----- 265

Qy 775 PIPTYFVVLTSCKNKHTPENCPGMIDVLPFIIPRPTVYESCEGKPKBALYVEBFRFA 834
Db 266 -----VII-----ESLWVEBLIKL 279

Qy 835 HIAVRDVEYLTGDLFYQDK 854
Db 280 HTARITDVEHTIGLSFYQQR 299

RESULT 15
A;Residues: 1-453 <NAcG>
A;Cross-references: GB:AB020686; NID:94240247; PIDN:BAA74902.1
A;Experimental source: adult brain
R:Gijssbers, R.; Ceulemans, H.; Stalmans, W.; Bollen, M.
DNA Res. 5, 355-364, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. XII. The complete
A;Reference number: A59389; MUID:99156230; PMID:10048485
A;Molecule type: mrNA
A;Content: annotation
R;Shalley, C.
Submitted to the EMBL Data Library, September 1999
A;Description: Contains actin, gamma pseudogene 9,
A;Reference number: A59391

RESULT 14
T33724 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) - Zymo
probable phosphodiesterase I (EC 3.1.4.1) / nucleotide pyrophosphatase / nucleotide diphosphatase (EC 3.6.1.9) - hu

C;Species: Zymomonas mobilis
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Aug-2002
C;Accession: T33724
R;Lee, J.S.; Jin, S.J.; Kang, H.L.; Kang, H.S.
submitted to the EMBL Data Library, August 1998
A;Description: Sequence analysis of 67R10 cosmid clone of Zymomonas mobilis 2M4.
A;Reference number: Z23392
A;Accession: T33724
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-429 <LEE>
A;Cross-references: EMBL:AF086791; NID:93820581; PIDN:AACT0363.1
C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Query Match 13.1%; Score 630.5.; DB 2.; Length 429;
Best Local Similarity 35.4%; Pred. No. 1e-36;
Matches 135; Conservative 143; Indels 27; Gaps 10;

Qy 160 PVIFSMDSFRAEVLTYWTDLMPNINLKTKTGFHNHYTIVTGLYPE 219
Db 49 PLILISIDESFRADYIKR--GLTNLVLASLAENGSYAKNMHPSPFSITFHNFYLTVTGLYPD 106
Qy 220 SRGILDDNNNNDVNL--NKGFLSLSKE-ONNPNAW-HGQPMLWLTAMYQLKAATYFWGSE 275
Db 107 HHG1VGNMNDDAHTPDSHPKMSDHOAATDRLWDEGEPWLTAEKGCVVSATMFWGESE 166
Qy 276 VATINSFPSIYMPYNGSYVPEEFERISTLKLWDLPKAERPRFTYMFEEFDSSGHAGGPVS 335
Db 167 ADISGRPRPMWQRDSSHVPSFSERVDFQFSWLYAPKKRPQFTLYFFNDVDAHGLYCPDS 226
Qy 336 ARVTKALQYDVAHFGMMLMEGLKORNLLNCVNILLADHGMDQTYCNKMEYMTDYFPRINF 395
Db 227 QEVNDNLVYKIDQTGIVQGLKORGIK--ANIVVSHGMATSSDDEVVANKILDESLY 284
Qy 396 FYM--YEGPAPRIRAKNIPHDFFSFNSEEIVRNLSCKRDPQHQFKRYLTDPDLPKRHYA 451
Db 285 HWTGGAAGAIEPS-SGHSLSKDLEPLASHD-----HMQCWPQKQOIPAFPHYG 331
Qy 452 KNRIDKYLFLVDQWLAVERSKS-NTRGCGNNGYNNBFRSMEAIFLAHGBPFEKEVE 510
Db 332 QNPVPRVYVCAAEVGWSLIMGDDMSMAAFAATKGNHGYDNQTPENGALFANGAFQKHKVIE 391
Qy 511 PFENIEVYNNMCDLRLIQDAP 531
Db 392 SMNDIVQPLVQVQLKLK-AP 411

RESULT 15
A;Residues: 1-453 <NAcG>
N;Alternate names: econucleotide pyrophosphatase/phosphodiesterase 4; KIAA0879 protein
C;Species: Homo sapiens (man)
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2002
C;Accession: A59389; B59391
R:Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosoawa, M.; Miyajima, N.; Tanaka, J. Biol. Chem. 276, 1361-1368, 2001
A;Title: Structural and catalytic similarities between nucleotide pyrophosphatases/phospho

A;Content: annotation
R;Shalley, C.
Submitted to the EMBL Data Library, September 1999
A;Description: Contains actin, gamma pseudogene 9,
A;Reference number: A59391

A;Accession: B59391
 A;Molecule type: DNA
 A;Residues: 1-453 <SMA>
 A;Cross-references: GB:AL035701; NID:95924008; PIDN:CAB56567.1
 C;Genetics:
 A;Gene: BNP4P4

A;Cap position: 6p11.2-6p21.1
 A;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
 C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase
 F;70/Active site: Thr #status predicted

Query Match	Score	DB 1:	Length
Best Local Similarity	35.5%	Pred. No.	1.3e-36;
Matches 139; Conservative	76;	Mismatches	23;
		Indels	23;
		Gaps	12;
QY	158 LPP-VILESMGDGERAELYTWTDLMPNINKLKGIGHSKYMARMAYPTKTFPHYTIVTG 216		
Db	24 LPPKHLVSSDGFRADYLKNEYE--FPHLQNFKEGVLTTEHVKNVFITTFPHYSIVTGL 81		
QY	217 YPESHGIDINMYDVNLANKFSLSKEQNPNPAWTH-GQPMLTAMYGQLKATYFPGS 274		
Db	82 YEESHGIVANSMYDAVTKCHFSDSN--DKDPWNNEAPBIVTNOLQENRSSAAAMPGT 139		
QY	275 EVAINGSFPSIYMPYNGSVFDPKAFR-REFTYMFPEPDSSGHAGGP 333		
Db	140 DVPIHDTISSYFVNNTSYFVNNTSYFVNNTMWLN-NSNPVPUTLYBEPDASGHXGP 197		
QY	334 V-SARVKALQVVDHAFCMLMEGKLRNQNLKRNQNLHCNVNILLADHGMDQTYCNCMEYMTDYFPR 392		
Db	198 EDKENNSRVLKIDDLDGIVQRLEMGLGWENLNVIIRSDHGMQCSDRLNLDSCDH 257		
QY	393 INFEMYEGPAPRIRAHNIPHDFFSFNSSEEIVRNLSCKPDKHFKPYLTPDLPKRLHYAK 452		
Db	258 SYTTIDLSPVAAI---LP---KINRTVEYNKLKNCSPP--HMNVYKEDIPNRFYQH 307		
QY	453 NVRIDKVLFLFDQOWLAVRSKSNTNCGGGNHGYNNEFRSMEAFLAHGPSFREKTEVEPF 512		
Db	308 NDRIQPIILVADEGNTIVLINESSORL-CDHGVDNSLPSMHPFLAAHGSFAFHKGKYKISTI 365		
QY	513 ENIEVNLMDLLRQAPAPNINGTHGSNLHIL 543		
Db	366 NIVDIYPMAMCHILGKPHPNNGTfGHTKCIL 396		

Search completed: July 6, 2004, 13:20:28
 Job time : 29 secs

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